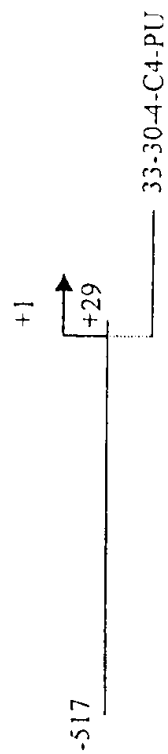
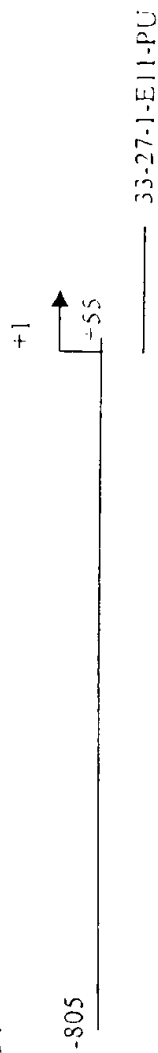


Promoter P13H2



Promoter P15B4



Promoter P29B6

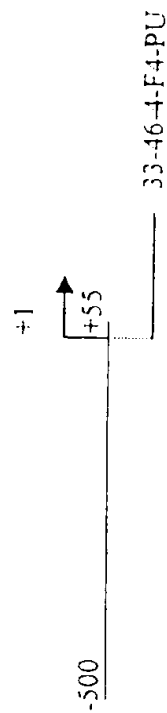


Figure 4

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME : GENSET SA
- (B) STREET : 24, RUE ROYALE
- (C) CITY: PARIS
- (E) COUNTRY : FRANCE
- (F) POSTAL CODE (ZIP) : 75008

(ii) TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
EXPRESSED IN PROSTATE

(iii) NUMBER OF SEQUENCES: 593

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy Disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: Win95
- (D) SOFTWARE: Word

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(ix) FEATURE:

- (A) NAME/KEY: Cap
- (B) LOCATION: 1
- (D) OTHER INFORMATION: m7Gppp added to 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCAUCCUAC UCCCAUCCAA UCCACCCUA ACUCCUCCCA UCUCCAC

47

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GCAUCCUACU CCAUCCAAU UCCACCCUAA CUCCUCCCAU CUCCAC

46

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATCAAGAATT CGCAGGAGAC CATTA

25

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TAATGGTCTC GTGCGAATTC TTGAT

25

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCGACAAGAC CAACGTCAAG GCCGC

25

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TCACCAGCAG GCAGTGGCTT AGGAG

25

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AGTGATTCCT GCTACTTTGG ATGGC

25

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCTTGGTCTT GTTCTGGAGT TTAGA

25

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TCCAGGATGG GAGACAAGCC AATTT

25

(2) INFORMATION FOR SEQ ID NO: 10:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AGGGAGGAGG AAACAGCGTG AGTCC

25

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGGGAAAGG AAAAGACTCA TATCA

25

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AGCAGCAACA ATCAGGACAG CACAG

25

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATCAAGAATT CCCACGAGAC CATTA

25

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ATCGTTGAGA CTCGTACCAG CAGAGTCACG AGAGAGACTA CACGGTACTG GTTTTTTTTT 60

TTTTTVN 67

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CCAGCAGAGT CACGAGAGAG ACTACACGG

29

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CACGAGAGAG ACTACACGGT ACTGG

25

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 526 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(261..376)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 166..281
 id N70479
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(380..486)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 54..160
 id N70479
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(110..145)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 403..438
 id N70479
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(196..229)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 315..348
 id N70479
 est
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 90..140
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.2
 seq LLLITAILAVAVG/FP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AAATATRAPAC AGCTACAATA TTCCAGGGCC ATCTCACTTGC CATTTCCTCAT AACAGCGTCA 60
GAGAGAAAGA ACTGACTGAR ACGTTTGAG ATG AAG AAA GTT CTC CTC CTG ATC 113

```

Met Lys Lys Val Leu Leu Leu Ile
-15 -10

ACA GCC ATC TTG GCA GTG GCT GTW GGT TTC CCA GTC TTT CAA GAC CAG 161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
-5 1 5

GAA CGA GAA AAA AGA AGT ATC AGT GAC AGC GAT GAA TTA GCT TCA GGR 209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
10 15 20

WTT TTT GTG TTC CCT TAC CCA TAT CCA TTT CGC CCA CTT CCA CCA ATT 257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
25 30 35

CCA TTT CCA AGA TTT CCA TGG TTT AGA CST AAN TTT CCT ATT CCA ATA 305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile
40 45 50 55

CCT GAA TCT GCC CCT ACA ACT CCC CTT CCT AGC GAA AAG TAAACAARAA 354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
60 65

GGAAAAGTCA CRATAAACCT GGTACCTIGA AATTGAAATT GAGUCASTTC CTTGAARAAT 414

CAAAATTCCT GTTAATAAAA RAAAAACAAA TGTAATTGAA ATAGCACACA GCATTCTCTA 474

GTCAATATCT TTAGTGATCT TCTTTAATAA ACATGAAAGC AAAAAAAAAA AA 526

```

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..17
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.2
seq LLLITAILAVAVG/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
1 5 10 15
Gly

```

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 260..464
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 153..357
id H57434
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..184
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 98..164
id H57434
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 56..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 35..92
id H57434
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 454..485
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 348..379
id H57434
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..545
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..428
id N27248
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 65..369
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 41..345
id H94779
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 61..399
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 6..344
id H09880
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 408..458
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 355..405
id H09880
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 60..399
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 56..395
id H29351
est

(ix) FEATURE:
(A) NAME/KEY: other
(B) LOCATION: 393..432
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 391..430
id H29351
est

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 346..408
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq SFLPSALVIWTSA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ACTCCTTTTA GCATAGGGGC TTCGGCGCCA GCGGCCAGCG CTAGTCGGTC TGSTAAGTGG	60
CTGATGCCGA GTTCGGTCTC TCGCGTCTTT TCCTGGTCCC AGGCAAAGCG GASGNAGATC	120
GTCAAACGGC CTAGTGCTTC GCGCTTCCGG AGAAAATCAG CGGTCTAATT AATTCCTCTC	180
GTTTGTTGAA SCAGTTACCA AGAATCTTCA ACCCTTTCCC ACAAAAGCTA ATTGAGTACA	240

```

CGTTCCTGTT GASTACACST TCCTGTTGAT TTACAAAAGG TGCAGGTATG AGCAGGTCTG 300
AAGACTAACA TTTTGTGAAG TTGTAAAACA GAAAACCTGT TAGAA ATG TGG TGG TTT 357
                                         Met Trp Trp Phe
                                         -20

CAG CAA GGC CTC AGT TTC CTT CCT TCA GCC CTT GTA ATT TGG ACA TCT 405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
      -15                      -10                      -5

GCT GCT TTC ATA TTT TCA TAC ATT ACT GCA GTA ACA CTC CAC CAT ATA 453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
      1                      5                      10                      15

GAC CCG GCT TTA CCT TAT ATC AGT GAC ACT GGT ACA GTA GGT CCA RAA 501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa
      20                      25                      30

AAA TGC TTA TTT GGG GCA ATG CTA AAT ATT GCG GCA GTT TTA TGT CAA 549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
      35                      40                      45

AAA TAGAAATCAG GAARATAATT CAACTTAAAG AAKTTCATTT CATGACCAAA 602
Lys

CTCTTCARAA ACATGTCTTT ACAAGCATAT CTCTTGTATT GCTTTCTACA CTGTTGAATT 662

GTCIGGCAAT ATTTCTGCAG TGGAAAATTT GATTIARMTA GTTCTTGACT GATAAATATG 722

GTAAGGTGGG CTTTTCCCCC TGTGTAATTG GCTACTATGT CTTACTGAGC CAAGTTGTAW 782

TTTGAAATAA AATGATATGA GAGTGACACA AAAAAAAAAA 822

```

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..21
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq SFLPSALVIWTS/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```

Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
      1                      5                      10                      15

```

Ile Trp Thr Ser Ala
20

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(103..398)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..296
id AA442893
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 185..295
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LSYASSALSPLT/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

ATCACCTTCT TCTCCATCCT TSTCTGGGCC AGTCCCCARC CCAGTCCCTC TCCTGACCTG      60
CCCAGCCCAA GTCAGCCTTC AGCAGCGCCT TTTCTGCACA CAGATATTCC AGGCCTACCT      120
GGCATTCCAG GACCTCCGMA ATGATGCTCC AGTCCCTTAC AAGCGCTTCC TGGATGAGGG      180
TGGC ATG GTG CTG ACC ACC CTC CCC TTG CCC TCT GCC AAC AGC CCT GTG      229
Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
      -35                      -30                      -25

AAC ATG CCC ACC ACT GGC CCC AAC AGC CTG AGT TAT GCT AGC TCT GCC      277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
      -20                      -15                      -10

CTG TCC CCC TGT CTG ACC GCT CCA AAK TCC CCC CGG CTT GCT ATG ATG      325
Leu Ser Pro Cys Leu Thr Ala Pro Xaa Ser Pro Arg Leu Ala Met Met
      -5                      1                      5                      10

CCT GAC AAC TAAATATCCT TATCCAAATC AATAAARWRA RAATCCTCCC TCCAAAGGG      384
Pro Asp Asn

TTTCTAAAAA CAAAAA AAA A      405

```


(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: AMINO ACID
 (C) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 1..37
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.9
 seq LSYASSALSPCLT/AP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
 1 5 10 15

Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
 20 25 30

Ser Pro Cys Leu Thr
 35

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 496 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 149..331
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..183
 id AA397994
 est
- (ix) FEATURE:
 (A) NAME/KEY: other

(B) LOCATION: 328..485
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 179..336
 id AA397994
 est

(1x) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(182..496)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 14..328
 id AA399680
 est

(1x) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 196..240
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.5
 seq ILSTVTALTFAXA/LD

(1) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

AAAAAATTGG TCCAGTTTT CACCCTGCCG CAGGGCTGGC TGGGGAGGGC AGCGGTTTAG      60
ATTAGCCGTG GCCTAGGCCG TTAAACGGGG TGACACGAGC NTGCAGGGCC GAGTCCAAGG      120
CCCGGAGATA GGACCAACCG TCAGGAATGC GAGGAATGTT TTTCTTCGGA CTCTATCGAG      180
GCACACAGAC AGACC ATG GGG ATT CTG TCT ACA GTG ACA GCC TTA ACA TTT      231
          Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
          -15                      -10                      -5

GCC ARA GCC CTG GAC GGC TGC AGA AAT GGC ATT GCC CAC CCT GCA AGT      279
Ala Xaa Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
          :                      5                      10

GAG AAG CAC AGA CTC GAG AAA TGT AGG GAA CTC GAG ASC ASC CAC TCG      327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Xaa Xaa His Ser
          15                      20                      25

GCC CCA GGA TCA ACC CAS CAC CGA AGA AAA ACA ACC AGA AGA AAT TAT      375
Ala Pro Gly Ser Thr Xaa His Arg Arg Lys Thr Thr Arg Arg Asn Tyr
          30                      35                      40                      45

TCT TCA GCC TGAAATGAAC CCGGGATCAA ATGGTTGCTG ATCARAGCCC ATATTTAAAT      434
Ser Ser Ala

TGGAAAAGTC AAATTGASCA TTATTAAATA AAGCTTGTTT AATATGTCTC AAACAAATAA      494
AA                                                                 496
  
```

(2) INFORMATION FOR SEQ ID NO: 24:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 1..15
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.5
 seq ILSTVTALTFAXA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Met	Gly	Ile	Leu	Ser	Thr	Val	Thr	Ala	Leu	Thr	Phe	Ala	Xaa	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 623 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 49..96
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.1
 seq LVLTLCCTLPLAVA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AAAGATCCCT	GCAGCCCGGC	AGGAGAGAAG	GCTGAGCCTT	CTGGCGTC	ATG GAG AGG	57
					Met Glu Arg	
					-15	
CTC GTC CTA ACC CTG TGC ACC CTC CCG CTG GCT GTG GCG TCT CCT GGC	105					
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly						
-10 -5 1						
TGC GCC ACG ACG CCA GCT CGC AAC CTG ACC TGC TAC CAG TGC TTC AAG	153					
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys						
5 10 15						
GTC AGC ACC TGG ACG GAG TGC CCG CCC ACC TGG TGC ACC CCG CTG GAC	201					

```

Val Ser Ser Trp Thr Glu Cys Pro Pro Thr Trp Cys Ser Pro Leu Asp
20          25          30          35
CAA GTC TGC ATC TCC AAC GAG GTC GTC GTC TCT TTT AAA TGG AGT GTA      249
Gln Val Cys Ile Ser Asn Glu Val Val Val Ser Phe Lys Trp Ser Val
          40          45          50
CGC GTC CTG CTC AGC AAA GGC TGT GCT CCC AGA TGT CCC AAC GAC AAC      297
Arg Val Leu Leu Ser Lys Arg Cys Ala Pro Arg Cys Pro Asn Asp Asn
          55          60          65
ATG AAK TTC GAA TGG TCG CCG GGC CCC ATG CTG CAA GGC GTG ATC ACC      345
Met Xaa Phe Glu Trp Ser Pro Ala Pro Met Val Gln Gly Val Ile Thr
          70          75          80
AGG CGC TGC TGT TCC TGG GCT CTC TGC AAC AGG GCA CTG ACC CCA CAG      393
Arg Arg Cys Cys Ser Trp Ala Leu Cys Asn Arg Ala Leu Thr Pro Gln
          85          90          95
GAG GGG CGC TGG GCC CTG CRA GGG GGG CTC CTG CTC CAG GAC CCT TCG      441
Glu Gly Arg Trp Ala Leu Xaa Gly Gly Leu Leu Leu Gln Asp Pro Ser
100          105          110          115
AGG GGC ARA AAA ACC TGG GTG CCG CCA CAG CTG GGG CTC CCA CTC TGC      489
Arg Gly Xaa Lys Thr Trp Val Arg Pro Gln Leu Gly Leu Pro Leu Cys
          120          125          130
CTT CCC AWT TCC AAC CCC CTC TGC CCA RGG GAA ACC CAG GAA GGA      534
Leu Pro Xaa Ser Asn Pro Leu Cys Pro Xaa Glu Thr Gln Glu Gly
          135          140          145
TAACACTGTG GGTCGCCCA CCGTGTGATT GGGACCACRA CTTCAACCCTC TTGGARACAA      594
TAAACTCTCA TGCCCCCAAA AAAAAAAAAA      623

```

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..16
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.1
seq LVLTLCTLPLAVA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

Met Glu Arg Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala
1          5          10          15

```

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 32..73
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7
seq LWLLFFLVTAIHA/EL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

AACTTTGCCT TGTGTTTTCC ACCCTGAAAG A ATG TTG TGG CTG CTC TTT TTT CTG      55
                               Met Leu Trp Leu Leu Phe Phe Leu
                               -10

GTG ACT GCC ATT CAT GCT GAA CTC TGT CAA CCA GGT GCA GAA AAT GCT      103
Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn Ala
-5                               1                               5                               10

TTT AAA GTG AGA CTT AGT ATC AGA ACA GCT CTG GGA GAT AAA GCA TAT      151
Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr
15                               20                               25

GCC TGG GAT ACC AAT GAA GAA TAC CTC TTC AAA GCG ATG GTA GCT TTC      199
Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe
30                               35                               40

TCC ATG AGA AAA GTT CCC AAC AGA GAA GCA ACA GAA ATT TCC CAT GTC      247
Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val
45                               50                               55

CTA CTT TGC AAT GTA ACC CAG AGG GTA TCA TTC TGG TTT GTG GTT ACA      295
Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr
60                               65                               70

GAC CCT TCA AAA AAT CAC ACC CTT CCT GCT GTT GAG GTG CAA TCA GCC      343
Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala
75                               80                               85                               90

ATA AGA ATG AAC AAG AAC CGG ATC AAC AAT GCC TTC TTT CTA AAT GAC      391
Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp
95                               100                               105

CAA ACT CTG GAA TTT TTA AAA ATC CCT TCC ACA CTT GCA CCA CCC ATG      439

```

Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro Met
 110 115 120

GAC CCA TCT GTG CCC ATC TGG ATT ATT ATA TTT GGT GTG ATA TTT TGC 487
 Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe Cys
 125 130 135

ATC ATC ATA GTT GCA ATT GCA CTA CTG ATT TCA TCA GGG ATC TGG CAA 535
 Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp Gln
 140 145 150

CGT ADA ARA AAG AAC AAA GAA CCA TCT GAA GTG GAT GAC GCT GAA RAT 583
 Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu Xaa
 155 160 165 170

AAK TGT GAA AAC ATG ATC ACA ATT GAA AAT GGC ATC CCC TCT GAT CCC 631
 Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp Pro
 175 180 185

CTG GAC ATG AAG GGA GGG CAT ATT AAT GAT GCC TTC ATG ACA GAG GAT 679
 Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu Asp
 190 195 200

GAG AGG CTC ACC CCT CTC TGAAGGGCTG TTGTTCTGCT TCCTCAARAA 727
 Glu Arg Leu Thr Pro Leu
 205

ATTAAACATT TGTCTCTGIG TGACTGCTGA GCATCCTGAA ATACCAAGAG CAGATCATAT 787

WTTTGTGTTT ACCATTCTTC TTTTGTAATA AATTTTGAAT GTGCTTGAAA AAAAAAAAAA 847

C 848

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..14
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7
 seq LWLLFFLVTAIHA/EL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GGGAAGATGG AGATAGTATT GCCTG

25

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: SINGLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTGCCATGTA CATGATAGAG AGATTC

26

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 546 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE:
 (A) NAME/KEY: promoter
 (B) LOCATION: 1..517

- (ix) FEATURE:
 (A) NAME/KEY: transcription start site
 (B) LOCATION: 518

- (ix) FEATURE:
 (A) NAME/KEY: TF binding-site
 (B) LOCATION: 17..25
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name CMYB_01
 score 0.983
 sequence TGTCAGTTG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(18..27)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MYOD_Q6
score 0.961
sequence CCCAACTGAC

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(75..85)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name S8_01
score 0.960
sequence AATAGAATTAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 94..104
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name S8_01
score 0.966
sequence AACTAAATTAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(129..139)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name DELTAEF1_01
score 0.960
sequence GCACACCTCAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(155..165)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA_C
score 0.964
sequence AGATAAATCCA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 170..178
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name CMYB_01
score 0.958
sequence CTTCAGTTG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 176..189
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA1_02
score 0.959
sequence TTGTAGATAGACA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 180..190
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA_C

score 0.953
sequence ACATAGGACAT

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 284..299
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name TAL1ALPHA47_01
score 0.973
sequence CATAACAGATGCTAAG

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 284..299
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name TAL1BETA47_01
score 0.983
sequence CATAACAGATGGTAAG

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 284..299
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name TAL1BETA1TF2_01
score 0.978
sequence CATAACAGATGGTAAG

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(287..296)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MYOD_Q6
score 0.954
sequence ACCATCTGTT

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(302..314)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name GATA1_04
score 0.953
sequence TCAAGATAAAGTA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 393..405
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name IK1_01
score 0.963
sequence AGTGGGAATTCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 393..404
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name IK2_01
score 0.985
sequence AGTGGGAATTCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site

(B) LOCATION: 396..405
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name CREL_01
 score 0.962
 sequence TGGGAATTCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
 (B) LOCATION: 423..436
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name GATA1_02
 score 0.950
 sequence TCAATGATATGGCA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
 (B) LOCATION: complement(478..489)
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name SRY_02
 score 0.951
 sequence TAAAACAAAACA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
 (B) LOCATION: 486..493
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name E2F_02
 score 0.957
 sequence TTTAGCGC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
 (B) LOCATION: complement(514..521)
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name MZF1_01
 score 0.975
 sequence TGAGGGGA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

TGAGTGGAGT GTTACATGTC AGTTGGGTTA AGTTTGTTAA TGTCAATCAA ATCTTCTATG   60
TCTTGATTGG CCTGCTAATT CTATTATTTC TGGAACTAAA TTAGTTTGAT GGTCTATTA   120
GTTATTGACT GAGGTGTGCT AATCTCCCAT TATGTGGATT TATCTATTTC TTCAGTTGTA   180
GATAGGACAT TGATAGATAC ATAAGTACCA GGACAAAAGC AGGGAGATCT TTTTCCAAA   240
ATCAGGAGAA AAAAATGACA TCTGGAAAAC CTATAGGGAA AGGCATAACA GATGGTAAGG   300
ATACTTTATC TTGAGTAGGA GAGCCTTCCT GTGGCAACGT GGAGAGGGGA AGAGGTCGTA   360
GAATTGAGGA GTCAGCTCAG TTAGAAGCAG GGAGTTGGGA ATTCCGTTCA TGATATTAG   420
CATCAGTGAT ATGGCAAATG TGGGACTAAG GGTAGTGATC ACAGGCTTAA AATTGTGTGT   480
TTTGTTTTAG CGCTGCTGGG GCATCGCCTT GGGTCCCTTC AAAAATATTC CCATGAATCT   540
CTTCAT                                     546

```

(2) INFORMATION FOR SEQ ID NO: 32:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GTACGAGGGA CTGTGACCAT TGC

23

(2) INFORMATION FOR SEQ ID NO: 33:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTGTGACCAT TGCTCCCAAG AGAG

24

(2) INFORMATION FOR SEQ ID NO: 34:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 861 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 1..806

(ix) FEATURE:

- (A) NAME/KEY: transcription start site
- (B) LOCATION: 807

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(60..70)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name NFY_Q6
score 0.356
sequence GGACCAATCAT

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 70..77
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MZF1_01
score 0.962
sequence CCTGSSGA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 124..132
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name CMYB_01
score 0.994
sequence TGACCGTTG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(126..134)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name VMYB_02
score 0.985
sequence TCCAACGGT

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 135..143
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name STAT_01
score 0.968
sequence TTCCTGGAA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(135..143)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name STAT_01
score 0.951
sequence TCCACGGAA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(252..259)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MZF1_01
score 0.956
sequence TTGGGGGA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 357..369
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name IK2_01
score 0.965
sequence GAATGGGATTC

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 384..391
- (C) IDENTIFICATION METHOD: matinspector prediction

(D) OTHER INFORMATION: name MZF1_01
score 0.986
sequence AGAGGGGA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(410..421)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name SRY_02
score 0.955
sequence GAAACAAAACA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 592..599
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.960
sequence GAAGGGGA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 618..627
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MYOD_Q6
score 0.981
sequence AGCATCTGCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 632..642
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name DELTAEF1_01
score 0.958
sequence TCCCACCTCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(813..823)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name S8_01
score 0.992
sequence GAGGCAATTAT

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(824..831)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.986
sequence AGAGGGGA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TACTATAGGG CACGCSTGGT CGACGGCCGG GCTGTTCTGG AGCAGAGGGC ATGTCAGTAA 60
TGATTGGTCC CTGGGAAGG TGTGGCTGGC TCCAGCACAG TGAGGCATTT AGGTATCTCT 120
GGGTGACCGT TGGATTCCTG GAAGCAGTAG CTGTTCTGTT TGGATCTGGT AGGACACAGG 180

```

CTCAGAGGGG TAGGCAAGAG GGAAGGTCAG AGGAGAAGGS AGGSARGGCC CAGTCAGAGC 240
GGAGCATGCC TTCCCCAAC CCTGGCTTSC YCTTGGYMAM AGGGCGKTTY TGGGMACTTR 300
AAYTCAGGGG CCAASCAGAA SCACAGGCC AKTCNTGGCT SMAAGCACAA TAGCCTGAAT 360
GGGATTTGAG GTTAGNCAGG GTGAGAGGGG AGGCTCTCTG GCTTAGTTTT GTTTTGTTET 420
CCAAATCAAG GTAAGTTGCT CCGTTCTGCT ACGGGCCTTG GTCTTGGGTT GTCCTCAGCC 480
AGTCGGAACT CCTAGCACT TTCAGGAGAG TGGTTTTAGG CCGTGGGGC TGTTCGTTC 540
CAAGCAGTGT GAGAACATGG CTGGTAGAGG CTCTAGCTGT GTGCGGGGCC TGAAGGGGAG 600
TGGGTTCTCG CCGAAGAGC ATCTGCCAT TTCCACCTT CCCTTCTCCC ACCAGAAGCT 660
TGCCTGAGCT GTTGGACAA AAATCCAAAC CCCACTGGC TACTCTGGCC TGGCTTCAGC 720
TTGGAACCCA ATACCTAGGC TTACAGCCA TCCTGAGCCA GGGGCCTCTG GAAATCTCT 780
TCCTGATGGT CTTTAGGTT TGGGCACAAA ATATAATTGC CTCTCCCTC TCCATTTC 840
TCTCTGGGA SCAATGGTCA C 861

```

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```

CTGGGATGGA AGGCAAGTA 20

```

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

GAGACCACAC AGCTAGACAA 20

```

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 555 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
 (A) NAME/KEY: promoter
 (B) LOCATION: 1..500
- (ix) FEATURE:
 (A) NAME/KEY: transcription start site
 (B) LOCATION: 501
- (ix) FEATURE:
 (A) NAME/KEY: TF binding-site
 (B) LOCATION: 191..206
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name ARNT_01
 score 0.964
 sequence GGACTCACGTGCTGCT
- (ix) FEATURE:
 (A) NAME/KEY: TF binding-site
 (B) LOCATION: 193..204
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name NMYC_01
 score 0.965
 sequence ACTCACGTGCTG
- (ix) FEATURE:
 (A) NAME/KEY: TF binding-site
 (B) LOCATION: 193..204
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name USF_01
 score 0.985
 sequence ACTCACGTGCTG
- (ix) FEATURE:
 (A) NAME/KEY: TF binding-site
 (B) LOCATION: complement(193..204)
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name USF_01
 score 0.985
 sequence CAGCACGTGAGT
- (ix) FEATURE:
 (A) NAME/KEY: TF binding-site
 (B) LOCATION: complement(193..204)
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name NMYC_01
 score 0.956
 sequence CAGCACGTGAGT
- (ix) FEATURE:
 (A) NAME/KEY: TF binding-site
 (B) LOCATION: complement(193..204)
 (C) IDENTIFICATION METHOD: matinspector prediction

(D) OTHER INFORMATION: name MYCMAX_02
score 0.972
sequence CAGCACGTGAGT

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 195..202
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name USF_C
score 0.997
sequence TCACGTGC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(195..202)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name USF_C
score 0.991
sequence GCACGTGA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(210..217)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.968
sequence CATGGGGA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 397..410
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name ELK1_02
score 0.963
sequence CTCTCCGGAAGCCT

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 400..409
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name CETS1P54_01
score 0.974
sequence TCCGGAAGCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(460..470)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name AP1_Q4
score 0.963
sequence AGTGACTGAAC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(460..470)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name AP1FJ_Q2
score 0.961
sequence AGTGACTGAAC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
 (B) LOCATION: 547..555
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name PADS_C
 score 1.000
 sequence TGTGGTCTC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```

CTATAGGGCA CGCKTGGTCG ACGGCCCGGG CTGGTCTGGT CTGKTGTGGA GTCGGGTTGA   60
AGGACAGCAT TTGKACATC TGGTCTACTG CACCTTCCCT CTGCCGTGCA CTTGGCCTTT   120
KAWAAGCTCA GCACCGGTGC CCATCACAGG GCCGGCAGCA CACACATCCC ATTACTCAGA   180
AGGAACTGAC GGACTCACGT GCTGCTCCGT CCCCATGAGC TCAGTGGACC TGTCTATGTA   240
GAGCAGTCAG ACAGTGCCTG CCATAGAGTG AGAGTTCAGC CAGTAAATCC AAGTGATTGT   300
CATTCTCTGC TGCATTAGTA ACTCCCAACC TAGATGTGAA AACTTAGTTC TTTCTCATAG   360
GTTGCTCTGC CCATGGTCCC ACTGCAGACC CAGGCACTCT CCGGAAGCCT GGAATCACC   420
CGTGTCTTCT GCCTGCTCCC GCTCACATCC CACACTTGTG TTCAGTCACT GAGTTACAGA   480
TTTTGCCTCC TCAATTCTC TTGTCTTAGT CCCATCCTCT GTTCCCCTCG CCAGTTTGTG   540
TAGCTGTGTG GTCTC                                     555
  
```

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 16..84
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 11.4
 seq VLALLLFVHYSNG/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

ACTTCCTGGT GCTGC ATG GTG TTC GTG CAC CTG TAC CTG GGT AAC GTG CTG   51
      Met Val Phe Val His Leu Tyr Leu Gly Asn Val Leu
              -20                      -15
GGG CTG CTG CTC TTC GTG CAC TAC AGC AAC GGC GAC GAA AGC AGC GAT   99
  
```

Ala Leu Leu Leu Phe Val His Tyr Ser Asn Gly Asp Glu Ser Ser Asp
 -10 -5 1 5

CCC GGG CCC CAC CAC CGT GCC 120
 Pro Gly Pro Gln His Arg Ala
 10

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 202..288
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.3
seq FLLCIFLICALA/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

AAAAGTGGAA AATGGGAGGC ATGAAATACA TCTTTTCGTT GTTGTTCCTT CTTTGTCTAG 60
 AAGGAGGCAA AACAGAGCAA GTAAAACATT CAGAGACATA TTGCATGTTT CAAGACAAGA 120
 AGTACAGAGT GGGTGAGAGA TGGCATCCTT ACCTGGAACC TTATGGGTTG GTTTACTGCG 180
 TGAAGTGCAT CTGCTCAGAG A ATG GGA ATG TGC TTT GCA GCC GAG TCA GAT 231
 Met Gly Met Cys Phe Ala Ala Glu Ser Asp
 -25 -20
 GTC CAA ATG TTC ATT GCC TTT CTC CTG TGC ATA TTC CTC ATC TGT GCT 279
 Val Gln Met Phe Ile Ala Phe Leu Leu Cys Ile Phe Leu Ile Cys Ala
 -15 -10 -5
 GCC CTC GCT GCC CAG AAG AGT GGG 303
 Ala Leu Ala Ala Gln Lys Ser Gly
 1 5

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 203..280
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 11
seq VLFLFLFWGVSLA/GS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

AAGGATGCTA TGCAAGTCAC TAATAAAGGA AGACACGGAC AGATGAACTT AAAAGAGAAG   60
CTTTAGCTGC CAAAGATTGG GAAAGGGAAA GGMCAAAAAA GACCCCTGGG CTACACGGCG   120
TAGGTGCAGG GTTCTCTACT GCTGTTCTTT TATGCTGGGA GCTGTGGCTG TAACCAACTA   180
GGAAATAACG TATGCAGCAG CT ATG GCT GTC AGA GAG TTG TGC TTC TCA AGA   232
                Met Ala Val Arg Glu Leu Cys Phe Ser Arg
                -25                               -20

CAA AGG CAA GTC CTG TTT CTT TTT CTT TTT TGG GGA GTG TCC TTG GCA   280
Gln Arg Gln Val Leu Phe Leu Phe Leu Phe Trp Gly Val Ser Leu Ala
-15                               -10                               -5

GGT TCT GGG TTT GGA CGT TAT TCG GTG ACC GGG   313
Gly Ser Gly Phe Gly Arg Tyr Ser Val Thr Gly
1                               5                               10

```

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 117..170
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.7
seq LILLALATGLVGG/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

AAAAGCCAGC CTACCTGCTG TAGCTGCCGC CAGTTCCTTC TCCGCGCCA CTGAGCCCCC   60

```

```

AGAGCBNMAG CCCCAGAGCC TAGGAACCTG GGGTCCGCTC CTCCTCCCTC CAGGCC ATG   119
                                         Met
AGG ATT CTG CAG TTA ATC CTG CTT GCT CTG GCA ACA GGG CTT GTA GGG   167
Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly
      -15                      -10                      -5
GGA GAG ACC AGG ATC ATC AAG GGG TTC GAG TGC AAG CCT CAC TCC CAG   215
Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln
      1                      5                      10                      15
CCC TGG CAG GCA GCC CTG TTC GAG AAG ACC CGG CTA CTC TGT GGG GCG   263
Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala
                      20                      25                      30
ACG CTC ATC GCC CCC AGA TGG CTC CTG ACA GCA GCC CAC TGC CTC AAG   311
Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu Lys
                      35                      40                      45
CCC CGC TAC GGG                                           323
Pro Arg Tyr Gly
      50

```

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 94..147
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7
seq LILLALATGLVGG/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```

AACAGSTTGA GGTGGCTGCG GGACTGGAGG TCATCGGGCA GAGGTCTCAC AGCAGCCAAG   60
AAAGCTGGGG CCCGCTCCTC CCCCTCCAG GCC ATG AGG ATT CTG CAG TTA ATC   114
                                         Met Arg Ile Leu Gln Leu Ile
                                         -15
CTG CTT GCT CTG GCA ACA GGG CTT GTA GGG GCA GAG ACC AGG ATC ATC   162
Leu Leu Ala Leu Ala Thr Gly Leu Val Gly Gly Glu Thr Arg Ile Ile
      -10                      -5                      1                      5
AAT GGG TTC GAG TGC AAG CCT CAC TGC GAG CCC TGG CAG GCA GCC CTG   210

```

Lys Gly Phe Glu Cys Lys Pro His Xaa Gln Pro Trp Gln Ala Ala Leu
 10 15 20

TTC GAG AAG ACG CGG CTA CTC TGT GGG GCG ACG CTC ATC GCC CCC AGA 258
 Phe Glu Lys Thr Arg Leu Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg
 25 30 35

TGG CTC 264
 Trp Leu

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 23..112
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.6
seq SLLLAVLVFFLFA/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CTCTAGAACC CGACCCACCA CC ATG AGG TCC TGC CTG TGG AGA TGC AGG CAC 52
 Met Arg Ser Cys Leu Trp Arg Cys Arg His
 -30 -25

CTG AGC CAA GGC GTC CAG TGG TCC TTG CTT CTG GCT GTC CTG GTC TTC 100
 Leu Ser Gln Gly Val Gln Trp Ser Leu Leu Leu Ala Val Leu Val Phe
 -20 -15 -10 -5

TTT CTC TTC GCC TTG CCC TCT DNH AVT TRR KGD SCT CAA ACA AAG CCT 148
 Phe Leu Phe Ala Leu Pro Ser Xaa Xaa Xaa Xaa Xaa Gln Thr Lys Pro
 1 5 10

TCC AGG CAT CAA CGC ACA GAG AAC ATT AAA GAA AGG TCT CTA CWG TCC 196
 Ser Arg His Gln Arg Thr Glu Asn Ile Lys Glu Arg Ser Leu Xaa Ser
 15 20 25

CTG GCA AAG CCT AAG TCC CAG GCA CCC ACA AGG GCA AGG AGG ACA ACC 244
 Leu Ala Lys Pro Lys Ser Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr
 30 35 40

ATC TAT GCA GAG CCA GTG CCA GAG ARC AAT GCC CTC AAC ACA CAA ACC 292
 Ile Tyr Ala Glu Pro Val Pro Glu Asn Asn Ala Leu Asn Thr Gln Thr
 45 50 55 60

CAG CCC AAG GCC CAC ACC ACC GGA GAG AGA AGG AAA GGA 331

Gln Pro Lys Ala His Thr Thr Gly Asp Arg Arg Lys Gly
 65 70

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 167..220
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.6
seq XILLALATGLVGG/EI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

AATGTGGGAC GTGGCTTTGT TCTAATAAGA CGAAGGGTGG AGTGCAGGCT TGGAAAGCAG   60
GAGAGCTCAG CCTACGTCTT TAATCCTCCT GCCCACCCTT TGGRTTCTGT CTCCACTGGG  120
RCTCAAGASV AGGACCCTGG GGGCCCGCTC CTCCCCCTC CAGGCC ATG AGG ATT   175
                               Met Arg Ile
CTG CAG TKA ATC CTG CTT GCT CTG GCA ACA GGG CTT GTA GGG GGA GAG   223
Leu Gln Xaa Ile Leu Leu Ala Leu Ala Thr Gly Leu Val Gly Gly Glu
-15                -10                -5                1
ATC AGG ATC ATC AAG GGG TTC GAG TGC AAG CCT CAC TCC CAG CCC TGG   271
Ile Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser Gln Pro Trp
                    5                10                15
CAG GCA GCC CTG TTC GAG AAG ACG CGG CTA CTA CTG TGG GGC GAC GCT   319
Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Leu Trp Gly Asp Ala
                20                25                30
CAT CGC CCC CAG ATG GCT CCT GAC AGC ASC CCA CTG CCT CAA GCC CCG   367
His Arg Pro Gln Met Ala Pro Asp Ser Ser Pro Leu Pro Gln Ala Pro
                35                40                45
CTA CAT AGT TCA CCT GGG GCA GCA CAA CCT CCA GAA GGA               406
Leu His Ser Ser Pro Gly Ala Ala Gln Pro Pro Glu Gly
                50                55                60

```

(2) INFORMATION FOR SEQ ID NO: 45:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 35..148
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.4
seq LWLLLKLVTXWA/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

ATACGTGTTTA TAAGCAACCT TGGTTTITACA TAGT ATG TTG SAA GAG TGT GGG GCT    55
                               Met Leu Glu Glu Cys Gly Ala
                               -35

GGG GTT GAT TTA GGA TTT GGA GGT GTA AAG TTT GGC AGT GAG ACA CCA    103
Gly Val Asp Leu Gly Phe Gly Gly Val Lys Phe Ala Ser Glu Thr Pro
-30                -25                -20

AAC CTT CTC TGG CTG CTT TTA AAA CTK GTA AGT ACC YCT TGG GCT GTA    151
Asn Leu Leu Trp Leu Leu Lys Leu Val Ser Thr Xaa Trp Ala Val
-15                -10                -5                1

AGA GTG ACT TTG ATC ATA TTT AAC AAC CAG GCA AGG                    187
Arg Val Thr Leu Ile Ile Phe Asn Asn Gln Ala Arg
      5                10

```

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 249..317
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.2
seq RCLLLALVAESSS/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

ATCTACTATA AAATCGATAG AAAAAAAGT TCTTTATGGC TACTGGTGAAG CTTTATATCC 60
TGATACGCCT GAACCTGGCA GCCCACAGTC AGTGTGCTTG ATGACTCTTA SATTGAAAGA 120
CCGCTCTTCC AAAGACACGT GCCTGTGCTC TGCAAGTTT ATCTGCCATC TTGGAAGGCT 180
CAAAGCAGTT TCTTTCTGTT GCTGAAGATA CCAGTGACCA CAGAAGGGCT TTTACCCCT 240
TCTCCGTA ATG ATC GCT TGC AGC ATT AGA GAG TTG CAC AGA TGT CTK TTG 290
      Met Ile Ala Cys Ser Ile Arg Glu Leu His Arg Cys Leu Leu
              -20              -15              -10

TTA GCT TTG GTG GCG GAG TCA TCC TCA CAG ACC CAC GGG 329
Leu Ala Leu Val Ala Glu Ser Ser Ser Gln Thr His Gly
              -5              1

```

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 182..232
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.2
seq SLVLCLLSATVFS/LQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

AGTTTTTTCC AGCTCCTGGG CGAATCCGAC ATCTGTTTCA ACTCTCCGCC GAGGGCGAGC 60
AGGAGCGAGA GTGTGTCGAA TCTSCGAGTG AAGAGGGAAC SAGGGGAAAA GAAACAAAGC 120
CACAGACGCA ACTTGAGACT CCCGCATCCC AAAAGAAGCA CCAGATCAGC AAAAAAAGAA 180
G ATG GGC CCC CCG AGC CTC GTG CTG TGC TTG CTG TCC GCA ACT GTG TTC 229
      Met Gly Pro Pro Ser Leu Val Leu Cys Leu Leu Ser Ala Thr Val Phe
              -15              -10              -5

TCC CTG CAG GGT GGA AGC TCG GCG TTC CTG TCG CAC CAC CGC CCC GGG 277
Ser Leu Gln Gly Gly Ser Ser Ala Phe Leu Ser His His Arg Pro Gly
      1              5              10              15

```

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 17..121
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9
seq AMWWLLLWGVQLQX/XP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

AGATGTCCAG TTCCAG ATG CCT GGA CCC AGA GTG TGG GGG AAA TAT CTC TGG      52
      Met Pro Gly Pro Arg Val Trp Gly Lys Tyr Leu Trp
      -35                      -30                      -25

AGA AGC CCT CAC TCC AAA GGC TGT CCA GGC CCA ATG TGG TGG CTG CTT      100
Arg Ser Pro His Ser Lys Gly Cys Pro Gly Ala Met Trp Trp Leu Leu
      -20                      -15                      -10

CTC TGG GGA GTC CTC CAG GST TKG CCC AAC CCG GGG CTC CGT CCT CTT      148
Leu Trp Gly Val Leu Gln Xaa Xaa Pro Asn Pro Gly Leu Arg Pro Leu
      -5                      1                      5

GGC CAA AGA GCT ACC CCA GCA GCT GAC ATC CCC CGG GTA CCC AGA GCC      196
Gly Xaa Arg Ala Thr Pro Ala Ala Asp Ile Pro Arg Val Pro Arg Ala
      10                      15                      20                      25

GTA TGG CAA AGG CCA AGA GAG CAA CAC GGA CAT CAA GGC TCC AGA GGG      244
Val Trp Gln Arg Pro Arg Glu Gln His Gly His Gln Gly Ser Arg Gly
      30                      35                      40

CTT TGC TGT GAG GCT CGT CTT CCA GGA CTT CGA CCT GGA GCC GTC CCA      292
Leu Cys Cys Glu Ala Arg Leu Pro Gly Leu Arg Pro Gly Ala Val Pro
      45                      50                      55

GGA CTG TGC AGG GGA CTC TGT CAC AAT CTC ATT CGT CGG TTC GGA TCC      340
Gly Leu Cys Arg Gly Leu Cys His Asn Leu Ile Arg Arg Phe Gly Ser
      60                      65                      70

AAG CCA CTC GGG
Lys Pro Leu Gly
      75

```

(xii) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs

(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 151..216
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.8
seq LLTLALLGGPTWX/XK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```

AAGAGCCCCA CGGCCAGCTC CTCCTGTTC CCCTGGCGGG CCCTCGCTTC TTCCTTCTGG      60
ATGGGGGGCCC AGGGGGCCAG GAGAGTATAA ASGSWKDKG GARGGGTGCC CGGCACAACC      120
AGACGCCCAG TCACAGGCGA GAGCCCTGGG ATG CAC CGS CCA GAG GCC ATG CTG      174
                               Met His Arg Pro Glu Ala Met Leu
                               -20                               -15

CTG CTG CTC ACG CTT GCC CTC CTG GGG GGC CCC ACC TGG GMA SGG AAG      222
Leu Leu Leu Thr Leu Ala Leu Leu Gly Gly Pro Thr Trp Xaa Xaa Lys
                               -10                               -5                               1

ATG TAT GGC CCT GGA GGA GGC AAG TAT TTC AGC ACC ACT GAA GAC TAC      270
Met Tyr Gly Pro Gly Gly Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr
                               5                               10                               15

GAC CAT GAA ATC ACA GGG CTG CGG GTG TCT GTA GGT CKT CTC CTG GTG      318
Asp His Glu Ile Thr Gly Leu Arg Val Ser Val Gly Xaa Leu Leu Val
                               20                               25                               30

AAA AGT GTC CAG GTG AAA CTT GGA GAC TCC TGG GAC GTG AAA CTG GGA      366
Lys Ser Val Gln Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly
                               35                               40                               45                               50

GGC CTT AGG TGG GAA TAC CCA GGA AGT CAC CCT GCA GCC AGG CGA ATA      414
Gly Leu Arg Trp Glu Tyr Pro Gly Ser His Pro Ala Ala Arg Arg Ile
                               55                               60                               65

CAT CAC AAA AGT CTT TGT CGC TTC CAA GCT TTC CTC      450
His His Lys Ser Leu Cys Arg Phe Gln Ala Phe Leu
                               70                               75

```

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs
(2) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 5..49
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6
seq SVSLALLSGWVGS/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```
AGAC ATG GTA AGT GTG AGT TTA GCG CTG CTG TCC GGA TGG GTT GGT AGC      49
Met Val Ser Val Ser Leu Ala Leu Leu Ser Gly Trp Val Gly Ser
-15                      -10                      -5

AGA CAG GGT GGA GTA GGG TTA AGC ACA CTG GTC ACC TTA GCA TTG CTT      97
Arg Gln Gly Gly Val Gly Leu Ser Thr Leu Val Thr Leu Gly Leu Val
1                      5                      10                      15

TCC TGG TGC TGG AGA ATG GTT AGG ACA CAG GCC TTG GAA GGT TTT TTG      145
Ser Trp Cys Trp Arg Met Val Arg Thr Gln Ala Leu Gln Gly Phe Leu
20                      25                      30

AGT GTG AAA TAT TAC TCA GCG TTT TCT GCA GAC CTG                      181
Ser Val Lys Tyr Tyr Ser Ala Phe Ser Ala Asp Leu
35                      40
```

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 129..275
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq IVFLLLRVSPCLG/PS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```
AAGATATCAC TGTCTTGTTC TCACTTAGAT CCTACTTACA AAGTGAGGCT TATTACAGA      60
```

ATAAAGCCTT CCTTTAAAGC TTTATAATAA TCATATTTAT TAATAATGCT GTTGTSCATA 120
 CTTATAGT ATG CAT ATA TTC AGC ATA TGT TGC ATG TST TCA GAA TTA CAT 170
 Met His Ile Phe Ser Ile Cys Cys Met Xaa Ser Glu Leu His
 -45 -40

AAG ATG AAA TCC CTT TCA TTG CAA CTT GCA AGT GAG AAA AGA TCC TTA 218
 Lys Met Lys Ser Leu Ser Leu Gln Leu Ala Ser Glu Lys Arg Ser Leu
 -35 -30 -25 -20

GTG GCT CTG GTG GAA GAA ATA GTA TTT CTT CTT CTC AGG GTG TCT CCC 266
 Val Ala Leu Val Glu Glu Ile Val Phe Leu Leu Leu Arg Val Ser Pro
 -15 -10 -5

TGC CTT GGC CCC TCC CAB AAG CCC CGG 293
 Cys Leu Gly Pro Ser Xaa Lys Pro Arg
 1 5

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 258..308
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3
seq VSALLMAWFGVLS/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

AGCGCCGAGC TGACCGGGCG ACGCCGCGGG AGGTTCTGGA AACGCCGGGA GCTGCGAGTG 60
 TCCAGACATC CTTGTGGAAC CAGGCGTTGT KTTTCCTTGG CAGCTGCGGA GACCCGTGAT 120
 AATTCGTTAA CTAATTCAAC AAACGGGACC CTTCTGTGTG CCAGAAACCG CAAGCAGTTG 180
 CTAACCCAGT GGGACAGGCG GATTGGAAGA GCGGGAAGGT COTGGCCAG AGCASTGTGA 240
 CACTTCCCTC TGTGACC ATG AAA CTC TGG GTG TCT GCA TTG CTG ATG GCC 290
 Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala
 -15 -10

TGG TTT GST GTC CTG AGC TGT GTG CAG ACC GGG 323
 Trp Phe Gly Val Leu Ser Cys Val Gln Thr Gly
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 92..157
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3
seq LLLPLMLMSMVSS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

AGACCTGAGT CATCCCCAGG GATCAGGAGC CTCCAGCAGG GAACCTTCCA TTATATTCTT   60
CAAGCAACTT ACAGCTGCAC CGACAGTTGC G ATG AAA GTT CTA ATC TCT TCC   112
                               Met Lys Val Leu Ile Ser Ser
                               -20

CTC CTC CTG TTG CTG CCA CTA ATG CTG ATG TCC ATG GTC TCT AGC AGC   160
Leu Leu Leu Leu Leu Pro Leu Met Leu Met Ser Met Val Ser Ser Ser
-15                -10                -5                1

CTG AWT CSA GGG GTC GCC AGA GGC CAC AGG GAC CGA GGC CAG GCT TCT   208
Leu Xaa Pro Gly Val Ala Arg Gly His Arg Asp Arg Gly Gln Ala Ser
      5                10                15

AGG AGA TGG CTC CAG GAA GGC GGA CTG   235
Arg Arg Trp Leu Gln Glu Gly Gly Leu
      20                25

```

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: 159..224
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.3
 seq LLLPLMLMSMVSS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

ACTGTTCTCG CCTCAAATG GGAACGCTGA CCTGGGACTA AAGCATAGAC CACGAGGCTG    60
AGTATCCTGA CCGAGTCAT CCCAGGGAT CAGGAGCCTC CAGCAGGGAA CTTTCATTA    120
TATTCTTCAA GCAACTTACA GCTGCACCGA CAGTTGCG ATG AAA GTT CTA ATC TCT    176
                               Met Lys Val Leu Ile Ser
                               -20

TCC CTC CTC CTG TTG CTG CCA CTA ATG CTG ATG TCC ATG GTC TCT AGC    224
Ser Leu Leu Leu Leu Leu Pro Leu Met Leu Met Ser Met Val Ser Ser
-15                      -10                      -5

AGC CTG AAT CCA GGG GTC GCC AGA GGC CAC AGG GAC CGA GGC CAG GCT    272
Ser Leu Asn Pro Gly Val Ala Arg Gly His Arg Asp Arg Gly Gln Ala
  1                      5                      10                      15

TCT AGG AGA TGG CTC CAG GAA GGC GGC CAA GAA TGT SAG TGC AAA GAT    320
Ser Arg Arg Trp Leu Gln Glu Gly Gly Gln Glu Cys Glu Cys Lys Asp
                20                      25                      30

TGG TTC CTG AGA GCC CCG AGA AGA AAA TTC ATG ACA GTG TCT GCG    365
Trp Phe Leu Arg Ala Pro Arg Arg Lys Phe Met Thr Val Ser Gly
    35                      40                      45
  
```

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 99..140
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.2
seq LLLLQLSLPSPTS/SP

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

AAVAATGATG TCGCTGGGAA CTGCGTGCAT TTGAAAAGAT AGCAATCAAG CATTCTTTTC    60
AGAGCGGTGT TCACTTTTCA GCGGTTTGGT TTCTGCTG ATG GTT TTG CTC GTT CAA    116
  
```

Met Leu Leu Leu Leu Gln
-10

TTA TCT CTS CCT TCT CCC ACC TCC TCT CCG 146
Leu Ser Leu Pro Ser Pro Thr Ser Ser Pro
-5 1

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 25..75
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1
seq LSFKLLLLAVALG/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

AGCCCCTGCT GCTCTGGGCA GAGG ATG CTG AAG ATG CTC TCC TTT AAG CTG 51
Met Leu Lys Met Leu Ser Phe Lys Leu
-15 -10

CTG CTG CTG GCC GTG GCT CTG GGC TTC TTT GAA GGA GAT GCT AAG TTT 99
Leu Leu Leu Ala Val Ala Leu Gly Phe Phe Glu Gly Asp Ala Lys Phe
-5 1 5

GGG GAA 105
Gly Glu
10

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 138..203
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8
seq LLTLALLGXXXWA/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

AGCTCCTTCC TGTTCCCCTG GCGGCCCTC GCTTCTTCT TCTGGATGGG GGCCCAGGGG    60
GCCCAGGAGA GTATAAAGG CATGTGGAGG GTGCCCGCA CAACCAGACG CCCAGTCACA    120
GGGCGGAGAG CHSTGRG ATG CAC CGG CCA GAG GCC ATG CTG CTG CTG CTC    170
          Met His Arg Pro Glu Ala Met Leu Leu Leu Leu
          -20                      -15

ACG CTT GCC CTC CTG GGG GRC MCC AMC TGG GCA GGG AAG ATG TAT GGC    218
Thr Leu Ala Leu Leu Gly Xaa Xaa Xaa Trp Ala Gly Lys Met Tyr Gly
-10                      -5                      1                      5

CCT GGA GGA GGC AAG TAT TTC AGC ACC ACT GAA GAC TAC GAC CAT GAA    266
Pro Gly Gly Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu
          10                      15                      20

ATC ACA GGG CTG CGG GTG TCT GTA GGT CTT CTC CTG GTG AAA AGT GTC    314
Ile Thr Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val
          25                      30                      35

CAG GTG AAA CTT GGA GAC TCC TGG GAC GTG                                344
Gln Val Lys Leu Gly Asp Ser Trp Asp Val
          40                      45

```

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 58..105
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8
seq VSAVLCVCAAAWC/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

AAGAGCAGGG CTGCATTTC AGCAGGAGCT GCGAGCACAG TGCTGGCTCA CACCAAG    57

```



```

ATG CTC AAG GTG TCA GCC GTA CTG TGT GTG TGT GCA GCC GCT TGG TGC      105
Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Trp Cys
   -15                      -10                      -5

AGT CAG TCT CTC GCA GCT GGC GCG GCG GTG GCT GCA GCC GGG GCG CGG      153
Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly Gly Arg
   1                      5                      10                      15

TCG GAC GGC GGT AAT TTT CTG GAT GAT AAA CAA TGG CTC ACC ACA ATC      201
Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu Thr Thr Ile
                20                      25                      30

TCT CAG TAT GAC AAG GAA GTC GGA CAG TGG AAC AAA TTC CGA GAC GAT      249
Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys Phe Arg Asp Asp
                35                      40                      45

GAT TAT TTC CGC ACT GGG                                              257
Asp Tyr Phe Arg Thr Gly
   50

```

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 124..174
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq VLWLISFFTFTDG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

AAGCATAAGA AGTGATTGAG CCACAAGTAT ACTGAAGGAA GGGCTCCCTC GAGTTGTGGT      60
GTGAGAGAGAT AATCACCAG TCACAGACTA TGCACCCGAC TGCTGCTGTT CAGTCCAGGG      120

AAA ATG AAA GTT GGA GTG CTG TGG CTC ATT TCT TTC TTC ACC TTC ACT      168
Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr
   -15                      -10                      -5

GAC GGC CAC GGT GGC TTC CTG GGG AAA AAT GAT GGC ATC AAA ACA AAA      216
Asp Gly His Gly Gly Phe Leu Gly Lys Asn Asp Gly Ile Lys Thr Lys
   1                      5                      10

AAA GAA CTC ATT GTC AAT AAG AAA AAA CAT CTA GGC CTC GCG      258
Lys Glu Leu Ile Val Asn Lys Lys Lys His Leu Gly Leu Gly

```

15

20

25

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 155..202
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7
seq ILLDLICLLFITA/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```

ACTGAAATAG GAAAGTAAGA TTTATACCCA TTATTCAGCC AAAATCTGTT TTTCTTTAAC    60
TTCTACCCAT TGTTCCTAAG TCTGCCCTCT GGGGCTGTGTA GAAATAATG AAGATGATGT   120
TATTAATGAT AACCAGTGCT TGCTGTAACC AGTT ATG TGC ATT ATT TTA TTG GAT    175
                               Met Cys Ile Ile Leu Leu Asp
                               -15                               -10

TTA ATT TGT TTA CTC TTT ATA ACA GCA TGT GTG GGG                        211
Leu Ile Cys Leu Leu Phe Ile Thr Ala Cys Val Gly
          -5                               1

```

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 131..307
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6

seq FMVFGSFFPLISC/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

```

ACATGGATTG ATTTGTTATT TGGGGATTAA ATTAGGCAGG GCACATAGTA GGGCCTCCTT    60
GGATGTTTGA TGGCTGTTGA ATGAACGTAA GTGAATCTGT TCAGTTTTAG GGTTTTATTC    120
CATTTTTGAT ATG GAT TGT GCC AGT ATA TCT GTA AAG TTC ACT TCT ATG    169
      Met Asp Cys Ala Ser Ile Ser Val Lys Phe Thr Ser Met
                -55                      -50

GCT ACC ATG CAT GAC TTG AST CAG TTC TGG GCT TCT AGA GGA GAG GTT    217
Ala Thr Met His Asp Leu Ser Gln Phe Trp Ala Ser Arg Gly Glu Val
      -45                      -40                      -35

ACA AAC TGG TGG CCA GTA GGA CAA ACT ASC CTA CCA CTG TTT TAT TTG    265
Thr Asn Trp Trp Pro Val Gly Gln Thr Ser Leu Pro Leu Phe Tyr Leu
      -30                      -25                      -20                      -15

GCT TTC ATG GTG TTT GGT TCT TTT TTT CCT TTA ATT TCC TGC CAG CCC    313
Ala Phe Met Val Phe Gly Ser Phe Phe Pro Leu Ile Ser Cys Gln Pro
                -10                      -5                      1

GGG                                                                316
Gly

```

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 147..206
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq LVLFGITAGATG/AK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

ACTTTTGAC TAGCACTAGC AAGGAAGGGG GTGGGCGCT CTTCTTTTT CTCTTAGAAG    60
AGGGTTTAGC ACAGGTTTTT TCGTTCTCAC TTCCACACCA CCTTACCGCC TCCCGAUCCT    120
CGCTCTCCCC CTCCCGACCT ATCGTC ATG ACC GCC TCT CCG GAT TAC TTG GTG    173
      Met Thr Ala Ser Pro Asp Tyr Leu Val
                -20                      -15

```

```

GTG CTT TTT GGG ATC ACT GCT GGG GGC ACC GGG GGC AAG CTA GGC TCG      221
Val Leu Phe Gly Ile Thr Ala Gly Ala Thr Gly Ala Lys Leu Gly Ser
-10                      -5                      1                      5

GAT GAG AAG GAG TTG ATC CTG CTG TTC TGG AAA GTC GTG GAT CTN GCC      269
Asp Glu Lys Glu Leu Ile Leu Leu Phe Trp Lys Val Val Asp Leu Ala
10                      15                      20

AAC AAG AAG GTG GGA CAG TTG CAC GAA BKA HGN TTA GAC CCG ATC TGG      317
Asn Lys Lys Val Gly Gln Leu His Glu Xaa Xaa Leu Asp Arg Ile Trp
25                      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 46..90
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq CVLVLAAAAGAVA/VF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

AAGCGGCTGG TCCCGGAAG TTGGACGCAT GCGCCGTTTC TCTGC ATG GTG TGC GTT      57
Met Val Cys Val
-15

CTC GTT CTA GCT GCG GCC GCA GGA GCT GTG GCG GTT TTC CTA ATC CTG      105
Leu Val Leu Ala Ala Ala Ala Gly Ala Val Ala Val Phe Leu Ile Leu
-10                      -5                      1                      5

CGA ATA TGG GTA GTG CTT CGT TCC ATG GAC GTT ACG CCC CGG GAG TCT      153
Arg Ile Trp Val Val Leu Arg Ser Met Asp Val Thr Pro Arg Glu Ser
10                      15                      20

CTC AGT ATC TTG GTA GTG GCT GGG TCC GGT GGG CAT ACC ACT GAG ATC      201
Leu Ser Ile Leu Val Val Ala Gly Ser Gly Gly His Thr Thr Glu Ile
25                      30                      35

CTG AGG CTG CTT GGG AGC TTG TCC AAT GCC TAC TCA CCT AGA CAT TAT      249
Leu Arg Leu Leu Gly Ser Leu Ser Asn Ala Tyr Ser Pro Arg His Tyr
40                      45                      50

GTC ATT GCT GAC ACT GAT GAA ATG AGT GCC ACG      282
Val Ile Ala Asp Thr Asp Glu Met Ser Ala Thr

```

55

60

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 48..179
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.5
seq LMIPLLLTPITA/TS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```

ACAACTCAAG CCAGACAGGC AGCAATTCCA GACTCGAAAG AGGCCTT ATG AAG AAA      56
                                         Met Lys Lys

ACC GGG GAC GGG GGT ACT TTG AGC ACC GAG AGG ATA GGA GGG GCC GCT      104
Thr Gly Asp Gly Gly Thr Leu Ser Thr Glu Arg Ile Gly Gly Ala Ala
-40                               -35                               -30

CTC CTC AGC CTC CTG CTG AAG AGG ATG AAG ATG ACT TTG ATG ATA CCC      152
Leu Leu Ser Leu Leu Leu Lys Arg Met Lys Met Thr Leu Met Ile Pro
-25                               -20                               -15                               -10

TTG TTG CTA TTG ACA CCT ATA ACT GCG ACC TCC ACT TCA AGG TGG CCC      200
Leu Leu Leu Leu Thr Pro Ile Thr Ala Thr Ser Thr Ser Arg Trp Pro
-5                               1                               5

GAG ATC GGA GTA GTG GCT ATC CGC TCA CAA TTG AGG GCT TTG CAT ACC      248
Glu Ile Gly Val Val Ala Ile Arg Ser Gln Leu Arg Ala Leu His Thr
10                               15                               20

TGT GGT CAG GAG CCC GTG CCA GCT ATG GGG TCA GAA GGG GCC GCG      293
Cys Gly Gln Glu Pro Val Pro Ala Met Gly Ser Glu Gly Ala Ala
25                               30                               35

```

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 32..100

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.5
seq LTFLQLLLISSLP/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AGTAGACGCT CGGGCACCAG CMGCGGCPAG G ATG GAG CTG GGT TGC TGG ACG	52
Met Glu Leu Gly Cys Trp Thr	
-20	
CAG TTG GGG CTC ACT TTT CTT CAG CTC CTT CTC ATC TCG TCC TTG CCA	100
Gln Leu Gly Leu Thr Phe Leu Gln Leu Leu Leu Ile Ser Ser Leu Pro	
-15 -10 -5	
AGA GAG TAC ACA GTC ATT AAT GAA GCC TGC CCT GGA GCA GAG TGG AMT	148
Arg Glu Tyr Thr Val Ile Asn Glu Ala Cys Pro Gly Ala Glu Trp Xaa	
1 5 10 15	
ATC ATG TGT CGG GAG TGC TGT GAA TAT GAT CAG ATT GAG TGC GTC TGC	196
Ile Met Cys Arg Glu Cys Cys Glu Tyr Asp Gln Ile Glu Cys Val Cys	
20 25 30	
CCC GGA AAG AGG GAA GTC GTG GGT TAT ACC ATC CCT TGC TGC AGG AAT	244
Pro Gly Lys Arg Glu Val Val Gly Tyr Thr Ile Pro Cys Cys Arg Asn	
35 40 45	
GAG GMG AAT GAG TGT GAC TCC TGC CTG ATC CAC CCA GGT TGT ACC ATC	292
Glu Xaa Asn Glu Cys Asp Ser Cys Leu Ile His Pro Gly Cys Thr Ile	
50 55 60	
TTT GAA AAC TGC AMG AGC TGC CGM AAT GGC TCA TGG GGG GGT ACC TTG	340
Phe Glu Asn Cys Xaa Ser Cys Arg Asn Gly Ser Trp Gly Gly Thr Leu	
65 70 75 80	

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 112..192
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.2
 seq SLLFFLLLEGGXT/EQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

```

AAGACCTCGG AACGAGAGCG CCCCAGGGAG CTGGGAGCGG GTGCACGGCT GGCACACGGA    60
GAAGGCVAKK RCNNNNRCTT GAAGGTTCTG TCACCTTTTG CAGTGGTCCA A ATG AGA    117
                                     Met Arg
RAA AAG TGG AAA ATG GGA GGC ATG AAA TAC ATC TTT TCG TTG TTG TTC    165
Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu Leu Phe
-25                      -20                      -15                      -10
TTT CTT TTG CTA GAA GGA GGC KAA ACA GAG CAA GTR AMN CAT TCA GAG    213
Phe Leu Leu Leu Glu Gly Gly Xaa Thr Glu Gln Val Xaa His Ser Glu
                      -5                      1                      5
ACA TAT TGC ATG TTT CAA GAC AAG AAG TAC AGA GTG GGT GAG AGA TGG    261
Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp
                      10                      15                      20
CAT CCT TAC CTG GAA CCT TAT GGG TTG GTT TAC TGC GTG AAC TGC ATC    309
His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile
                      25                      30                      35
TGC TCA GAG RAT GGG AAT GTG CTT TGC AGC CGA GTC AGA TGT            351
Cys Ser Glu Xaa Gly Asn Val Leu Cys Ser Arg Val Arg Cys
40                      45                      50

```

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 68..124
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.2
 seq VSIMLLLVTVSDC/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

AAAGGCTGAG CCGGAGGAAG CGAGAGGCAT CTAAGCAGGC AGTGTTTTGC CTTACCCCA    60

```

```

AGTGACC ATG ASA GGT GCC ACG CGA GTC TCA ATC ATG CTC CTC CTA GTA    109
      Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val
                -15                      -10

ACT GTG TCT GAC TGT GCT GTG ATC ACA GGG GCC TGT GAG CGG GAT GTC    157
Thr Val Ser Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val
      -5                1                5                10

CAG TGT GGG GCA GGC ACC TGC TGT GCC ATC AGC CTG TGG CTT CGA GGG    205
Gln Cys Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly
                15                20                25

CTG CGG ATG TGC ACC CCG CTG GGG CGG GAA GGC GAG GAG TGC CAC CCC    253
Leu Arg Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro
                30                35                40

GGC AGC CAC AAG ATC CCC TTC TTC AGG AAA CGC AAG CAC CAC ACC TGT    301
Gly Ser His Lys Ile Pro Phe Phe Arg Lys Arg Lys His His Thr Cys
      45                50                55

CCT TGC TTG                                310
Pro Cys Leu
      60

```

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 240..302
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq SALLFSLICEAST/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

ACCTTTCTGG ACCTTGCAAA CTGTGACATA TAAAGCTGT TAGCTGCTCC TCTAGCCAGC    60
AGCATTCAAA CATTGCAGAG CTTTGCTCTC AGAGASTTTG TAAAAAGACA CACTCCTCTT   120
ACAAGAGTTC ATGCTACCAC ATAGCAAAGA ACCTTAAATT TTTGGAGAGAA CAATATATTC   180
ATTTTGGCAT TGTGCAGAGC AAGTAAACT CGGTGGCCTC TTCTTCTCCA CCCCTCAAR    239
ATG ATA GCR ATC TCT GCC GTC AGC AGT GCA CTC CTG TTC TCC CTT CTC    287
Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu

```


-20	-15	-10	
TGT GAA GCA AGT ACC GTC GTC CTA CTC AAT TCC ACT GAC TCA TCC CCG	335		
Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro			
-5 1 5 10			
CSA ACC AAT AAT TTC RCT GAT AWT GAA GCA GCT CTG AAA GCA CAT	380		
Xaa Thr Asn Asn Phe Xaa Asp Xaa Glu Ala Ala Leu Lys Ala His			
15 20 25			

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 181..243
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq SALLFSLCEAST/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

AGCATTCAAA CCTTGCAGAG CTTTGCTCTC AGAGAGTTTC TAAAAAGACA CACTCCTCTT	60
ACAAGAGTTC ATGCTACCAC ATAGCAAAGA ACCTTAAATT TTTGGAAGAA CAATATATTC	120
MATTTTGGCA TTGTGCAGAG CAAAGTAAAC TCGGTGGCCT CTTCTTCTCC ACCCCTCAAA	180
ATG ATA GCA ATC TCT GCC GTC AGC AGT GCA CTC CTG TTC TCC CTT CTC	228
Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu	
-20 -15 -10	
TGT GAA GCA AGT ACC GTC GTC CTA CTC AAT TCC ACT GAC TCA TCC CCG	276
Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro	
-5 1 5 10	
CCA ACC AAT AAT TTC ACT GAT ATT GAA GCA GCT CTG AAA GCA CAA TTA	324
Pro Thr Asn Asn Phe Thr Asp Ile Glu Ala Ala Leu Lys Ala Gln Leu	
15 20 25	
GAT TCA GCG GAT ATC CCC AAA GCC AGG CCG AAG CGC TAC ATT TCG CAG	372
Asp Ser Ala Asp Ile Pro Lys Ala Arg Arg Lys Arg Tyr Ile Ser Gln	
30 35 40	
AAT GAC ATG ATC GCC ATT GTT GAT TAT CAT AAT CAA GTT CGG GGC AAA	420
Asn Asp Met Ile Ala Ile Leu Asp Tyr His Asn Gln Val Arg Gly Lys	
45 50 55	

GTG TTC CCA MCG GCA
Val Phe Pro Xaa Ala
60

435

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 352..417
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq LLTLVLCVAVAYE/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

```

ATTGAGCTGT CTGCAGCAGA GCTGAGAGGA CCAGCCATTT TACTTATGGA AACAGTGTG   60
GCATATTCTG CTGAGCTTCG CCCTGGAAGA AGCCTCTTTT ATACATCTCT TCAGGGAAGA   120
GAGAAGCAAT GGGCATGTTA GTATACAATG ATCACAGCCA CGCAGGCCTG CAAGCTGCCT   180
TTTGGACAGG CTGTTGACTG CCGTTCCAAT TAGCTGATTG GAGAAATGTGG AATGCAGACT   240
GATAATGCTG CATATCTGCT ATCAGGCAGC AGCAAAGGTT TTTGTCTTGG GAAGGCAAGC   300
TTTCCTGCA ATATTATCTC AGCAGCTCCC TAGCTGCTTA CCCTGAAAAC G ATG GAT   357
                                     Met Asp
CCA AAC GGA GGG TGT TGC ACT CTG CTA ACG CTG GTC CTG TGC GTG GCT   405
Pro Asn Gly Gly Cys Cys Thr Leu Leu Thr Leu Val Leu Cys Val Ala
-20          -15          -10          -5
GTG GCA TAT GAG CGG CAG GAG                                     426
Val Ala Tyr Glu Arg Gln Glu
1

```

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 288..362
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.2
 seq LFTFSTSLPSSLS/SS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

```

ACAATACCTG TTACTTATAT ACTTTTCTTT GTCTAAAAAA GAAATAAGAT CTGTCTAGAT   60
GACTGATTAA CTTAGGGAGA TTCTGATTAA CAGAATTCTT AGAAATGGCT TTCAGCAGGC   120
AAAGASAAAA TTATATTTTG TACCAATTTA TATAAAGTTC ATCTAGCTCA GCTTTTGGAG   180
ATGTCCCTGG GGCTAGAGAT GAAATATCGT TTTCTGTCC ACAGACAGCG GTCTGCAGTT   240
CACCCCATGA ACTCATACAG GTCAGAATTA AACCCCGAGC TTTGTTT ATG GAG GGT   296
                                   Met Glu Gly
                                   -25

GAG ATA TAT TTC CAA GTA TTT CTT TCT CTT TTC ACA TTT TCC ACA TCA   344
Glu Ile Tyr Phe Gln Val Phe Leu Ser Leu Phe Thr Phe Ser Thr Ser
   -20               -15               -10

TTA CCA TCA TCA TTG TCG TCA TCA TCA TTG TCA TCA TCC AAT GGG   389
Leu Pro Ser Ser Leu Ser Ser Ser Ser Leu Ser Ser Ser Asn Gly
   -5               1               5

```

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 328 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 194..316
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7
 seq FLCMLAIDLALS/TS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```

ATGAGTCAGC CTGAAAGGAA CAGGCCGAAC TGCTGTATGG GCTCTACTGC CASTGTGACC   60
TCACCCCTCTC CAGTCACCCC TCCTCAGTTC CAGCTATGAG TTCCTGCAAC TTCACACATG  120
CCACCTTTGT GCTTAATKGG AATCCCAGGG ATTAGAGAAA GCCCATTCTT GGGTTGGCTT  180
CCCCCTCCTT TCC ATG TAT GTA GTG GCA ATG TTT GGA AAC TCC ATC GTG   229
      Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val
      -40                      -35                      -30
GTC TTC ATC GTA AGG ACG GAA CGC AGC CTG CAC GCT CCG ATG TAC CTC   277
Val Phe Ile Val Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu
      -25                      -20                      -15
TTT CTC TGC ATG CTT GCA GCC ATT GAC CTG GCC TTA TCC ACA TCC ACC   325
Phe Leu Cys Met Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr
      -10                      -5                      1
ATG
Met
328

```

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 79..207
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq PWFLAPWCPGTQS/NR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

ACGCTTCGTT CTGGTTCTGG TTCTAGTTCT GGTTCTAACA ACTCACAATC CCTTTAGCTT   60
TCTCTCCCTT CCCTTTGA ATG AGA GAA ACT AMC CCG CTT CCG AAG CCC CTG   111
      Met Arg Glu Thr Xaa Pro Leu Pro Lys Pro Leu
      -40                      -35
AAA GAC ACT GCT CCT TCC TCT CAT GGA GTT GGC TCC GAC AGC CCG TCT   159
Lys Asp Thr Ala Pro Ser Ser His Gly Val Gly Ser Asp Ser Pro Ser
      -30                      -25                      -20
GCC ACC AGG CCA TGG TTC CTT GCC CCA TGG TGT CCT GGG ACC CAG AGC   207
Ala Thr Arg Pro Trp Phe Leu Ala Pro Trp Cys Pro Gly Thr Gln Ser

```


Val Pro Gly

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 3..65
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq VILLFSYPSCCLC/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

AT ATG CAT TAT TTT GTT GCT GGG AAA GTA ATC CTT CTC TTC TCT TAT	47
Met His Tyr Phe Val Ala Gly Lys Val Ile Leu Leu Phe Ser Tyr	
-20 -15 -10	
CCA TCA TGT TGT TTG TGT TTC TTG GTG TAC AGG AGA GTA AGC WAT TTA	95
Pro Ser Cys Cys Leu Cys Phe Leu Val Tyr Arg Arg Val Ser Xaa Leu	
-5 1 5 10	
TTT AAG TGC TTT GAG	110
Phe Lys Cys Phe Glu	
15	

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 160..216
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7

seq STVVVLQVLQTQATS/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```

ACAGCCCARA CATGGCGTGT TCCTAGAAGC CGCTTTCGGC ATCAGTAGGC GCGGCGGTGG      60
GGTGTGGCAK CGTGGGGAGA GGGAMCAACC GACGCCACTT CGTGTGGGA ACTCGGAGCG      120
GGANRGCCGG GCAATTCCCG ACCGAACCAA ACGGTTTCC ATG GAT CTC AAT AGT      174
                               Met Asp Leu Asn Ser
                               -15

GCC AGC ACT GTT GTT CTT CAG GTG TTA ACA CAG GCC ACC AGT CAG GAT      222
Ala Ser Thr Val Val Leu Gln Val Leu Thr Gln Ala Thr Ser Gln Asp
                               -10                -5                1

ACT GCT GTG TTA AAA CCA GCT GAG GAG CAG TTG AAG CAG TGG GAG ACA      270
Thr Ala Val Leu Lys Pro Ala Glu Glu Gln Leu Lys Gln Trp Glu Thr
                               5                10                15

CAG CCA GGW TTC TAT TCA GTG TTG CTG AAT ATT TTC ACC AAC CAC GGG      318
Gln Pro Gly Phe Tyr Ser Val Leu Leu Asn Ile Phe Thr Asn His Gly
                               20                25                30

```

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 95..313
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq FLCMLAAIDLALS/TS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

```

ATGAGTCAGC CTGAAAGAAC AGGCCGAAC TGTGTATGGG CTCTACTGCC AGTGTGACCT      60
CACCCCTCTCC AGTCACCCCT CCTCAGTTCC AGCT ATG AGT TCC TGC AAC TTC ACA      115
                               Met Ser Ser Cys Asn Phe Thr
                               -70

CAT GCC ACC TTT GTG CTT ATT GGT ATC CCA GGA TTA GAG AAA GCC CAT      163
His Ala Thr Phe Val Leu Ile Gly Ile Pro Gly Leu Gln Lys Ala His
                               -65                -60                -55

```

```

TTC TGG GTT GGC TTC CCC CTC CTT TCC ATG TAT GTA GTG GCA ATG TTT      211
Phe Trp Val Gly Phe Pro Leu Leu Ser Met Tyr Val Val Ala Met Phe
-50                      -45                      -40                      -35

GGA AAC TGC ATC GTG GTC TTC ATC GTA AGG ACG GAA CGC AGC CTG CAC      259
Gly Asn Cys Ile Val Val Phe Ile Val Arg Thr Glu Arg Ser Leu His
                      -30                      -25                      -20

GCT CCG ATG TAC CTC TTT CTC TGC ATG CTT GCA GCC ATT GAC CTG GCC      307
Ala Pro Met Tyr Leu Phe Leu Cys Met Leu Ala Ala Ile Asp Leu Ala
                      -15                      -10                      -5

TTA TCC ACA TCC ACC ATG                                          325
Leu Ser Thr Ser Thr Met
1

```

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 179..346
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq PLFFSCSISATHS/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

```

ACAAAATCAA GAAATCCAA CATAGATGGT CAAAATATTC ATAGGTGACT GAGAGTATCC      60
AAATGGGCCA GGTGACTGAG AATACGCAAA CAGGCCAGAA TAATATCTGT GTTAAATTTG      120
ACCTCTATT TTATTAACAT ATCTGTCATG ACCTTTCTCT GTACCTGCTG TAGTACTC      178
ATG TAT AGA CTC AGT CTT ATA GCA GGC CCT GGG TCC TAT CCT GTG CTA      226
Met Tyr Arg Leu Ser Leu Ile Ala Gly Pro Gly Ser Tyr Pro Val Leu
-55                      -50                      -45

AGA TGG GGA GTT TGG GAC ATC CCT AGT TCA TTA GTT CAA GTG ACT TAC      274
Arg Trp Gly Val Trp Asp Ile Pro Ser Ser Leu Val Gln Val Thr Tyr
-40                      -35                      -30                      -25

CAT CAG CCC AAC CTC ACT ACA AAT TTG GAT CTG CCT TTG TTC TTC AGT      322
His Gln Pro Asn Leu Thr Thr Asn Leu Asp Leu Pro Leu Phe Phe Ser
20                      -15                      -10

TGT AGT ATC TCG GCT ACC CAT TCT TGT GTC AAG CCT CCA TCT GTA ATT      370

```


Cys Ser Ile Ser Ala Thr His Ser Cys Val Lys Pro Pro Ser Val Ile

ATT GGT ATC TCT TCT TTC CTG AGC TTT CCT TAT CAA ACT TTG GTA 415
Ile Gly Ile Ser Ser Phe Leu Ser Phe Pro Tyr Gln Thr Leu Val
10 15 20

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 128..199
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.9
seq LCFLLLLAVAMSFF/GS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

AAGTTGGTGA GCTTTTCCGG TGCTCTGCAC AGATGCTGGG GCGCTGAGCA AACAGCCCTC 60

AGTTTCTGGA GCTGTTCCGA GTCCCGTGGA GTCTCCATCT GAGCCCTTTC CTAGTCCAGG 120

CATCCCG ATG TTG GTG GAT GGC CCA TCT GAG CGG CCA GCC CTG TGC TTC 169
Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe
-20 -15

TTG CTG TTG GGT GTG GCA ATG TCT TTC TTC GGC TCA GCT CTA TCC ATA 217
Leu Leu Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile
-10 -5 1 5

GAT GAA ACA CGG GCG CAT CTG TTG TTG AAA GAA AAG ATG ATG CGG CTG 265
Asp Glu Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu
10 15 20

GGG GGG CGG CTG GTG CTC AAC ACC AAG GAG GAG CTG GCC AAT GAG AGG 313
Gly Gly Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg
25 30 35

CTC ATG ACG CTC AAA ATC GCT GAG ATG AAG GAG GCC ATG AGG ACC CTG 361
Leu Met Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu
40 45 50

ATA TTC CCA GCG AGC ATG CAC TTT TTC CAG GCC AAA TGG 400
Ile Phe Pro Pro Ser Met His Phe Phe Gln Ala Lys Trp
55 60 65

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 33..137
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq XLXXLLTPPPSYG/HQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

```

AACCGGCCCCG CGCCCCGCCA TGGAGGACCT GG ATG CCC TGC TCT CTG ACC TGG      53
                               Met Pro Cys Ser Leu Thr Trp
                               -35                               -30

AGA CTA CCA CCT CGC ACA TGC CAA KGT CAK GGG CTY CYA AAG AGC GYY      101
Arg Leu Pro Pro Arg Thr Cys Gln Xaa Xaa Gly Leu Xaa Lys Ser Xaa
      -25                               -20                               -15

CTT GYG GAB CTK CTC ACC CCT CCC CCA TCC TAT GGC CAC CAG CCA CAG      149
Leu Xaa Xaa Leu Leu Thr Pro Pro Pro Ser Tyr Gly His Gln Pro Gln
      -10                               -5                               1

ACA GGG TCT GGG GAG TCT DCA GGA GCC TCG GGG GAC AAG GAC CAC CTG      197
Thr Gly Ser Gly Glu Ser Xaa Gly Ala Ser Gly Asp Lys Asp His Leu
      5                               10                               15                               20

TAC AGC ACG GTA TGC                                          212
Tyr Ser Thr Val Cys
      25

```

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 15..137
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8
seq LFLFLTSIAEXCS/TP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

```

ACCCTGTKCT TKTC ATG GTT DTC TGG CTC GTC TTA TTT GCT CTT CAG ATT      50
           Met Val Xaa Trp Leu Val Leu Phe Ala Leu Gln Ile
           -40                      -35                      -30

TAC TCC TAT KKY AGT ACT CGA GAT CAG CCT GCA TCA CGT GAK AGG CTT      98
Tyr Ser Tyr Xaa Ser Thr Arg Asp Gln Pro Ala Ser Arg Xaa Arg Leu
           -25                      -20                      -15

CTT TTC CTT TTT CTG ACA AGT ATT GCG GAA TRC TGC AGC ACT CCT TAC      146
Leu Phe Leu Phe Leu Thr Ser Ile Ala Glu Xaa Cys Ser Thr Pro Tyr
           -10                      -5                      1

TCT CTT TTG GGT TTK GTC TTC ACG GTT TCT TTT GTT GCC TTG GGT GTT      194
Ser Leu Leu Gly Xaa Val Phe Thr Val Ser Phe Val Ala Leu Gly Val
           5                      10                      15

CTC ACA CTC TGC AAG TTT TAC TTG CAG GGT TAT CCA GCT TTC ATG AAT      242
Leu Thr Leu Cys Lys Phe Tyr Leu Gln Gly Tyr Arg Ala Phe Met Asn
           20                      25                      30                      35

GAT CCT GCC ATG AAT CGG GGA GGT GCG                                  269
Asp Pro Ala Met Asn Arg Gly Gly Ala
           40

```

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 9..62
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq LPLLXXXSLPVGA/WL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

AAGTCCTG ATG GCC CGG CAT GGG TTA CCG CTG CTG CHB YWG HTG TCG CTC 50
 Met Ala Arg His Gly Leu Pro Leu Leu Xaa Xaa Xaa Ser Leu
 -15 -10 -5

CCG GTC GGC GCG TGG CTC 68
 Pro Val Gly Ala Trp Leu
 1

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 258..368
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq ILYILWYCSVCSS/GS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

AAGGTTGGTC TGGACCGGAA GCGAAGATGG CGACTTCTGG CGCGGCCTCG GCGGASTGGT 60
 GATCGGCTGG TGCATATTCG GCCTCTTACT ACTGGCKATT TTGGCATTCT GCTGGATATA 120
 TGTTCGTAAG TACCAAAGTC GSCGGGAAAG TGAAGTTGTC TCCACCATAA CAGCAATTTT 180
 TTCTCTAGCA ATTGCACTTA TCACATCAGC ACTTCTACCA GTGGATATAT TTTTGGTTTC 240
 TTACATGAAA AATCAAAA ATG GTA CAT TTA AGG ACT GGG CTA ATG CTA ATG 290
 Met Val His Leu Arg Thr Gly Leu Met Leu Met
 -35 -30
 TCA GCA GAC AGA TTG AGG ACA CTG TAT TAT ACG GTT ACT ATA CTT TAT 338
 Ser Ala Asp Arg Leu Arg Thr Leu Tyr Tyr Thr Val Thr Ile Leu Tyr
 -25 -20 -15
 ATT CTG TGG TAT TGT TCT GTG TGT TCT TCT GGA TCC CTT TTG TCT ACT 386
 Ile Leu Trp Tyr Cys Ser Val Cys Ser Ser Gly Ser Leu Leu Ser Thr
 -10 -5 1 5
 TCT ATT ATG AAG AAA AGG ATG 407
 Ser Ile Met Lys Lys Arg Met
 10

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 196..240
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq ILSTVTALTFFARA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

```

AAAAAATTGG TCCAGTTTT CACCCTGCCG CAGGGCTGGC TGGGGAGGGC AGCGGTTTAC   60
ATTAGCCGTG GCCTAGGCCG TTAAACGGGG TGACACGAGC HTGCAGGGCC GAGTCCAAGG  120
CCCGGAGATA GCACCAACCG TCAGGAATGC GAGGAATGTT TTTCTTCGGA CTCTATCGAG  180
GCACACAGAC AGACC ATG GGG ATT CTG TCT ACA GTG ACA GCB TTA ACA TTT   231
      Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
      -15                -10                -5

GCC AGA GCC CTG GAC GGC TGC AGA AAT GGC ATT GCC CAC CCT GCA AGT   279
Ala Arg Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
      1                5                10

GAG AAG CAC AGA CTC GAG AAA TGT AGG GAA CTC GAG AGC AGC CAC TCG   327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Ser Ser His Ser
      15                20                25

GCC CCA-GGA TCA ACC CAG CAG                                     348
Ala Pro Gly Ser Thr Gln Gln
      30                35

```

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: 45..113
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.5
 seq LTFLQXLLISSLX/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```

ACTCTCCCTC CCCASTAGAC GCTCGGGCAC CAGCCGCGGC AAGG ATG GAG CTG GGT      56
                               Met Glu Leu Gly
                               -20

TGC TGG ACG CAG TTG GGG CTC ACT TTT CTT CAG STC CTT CTC ATC TCG      104
Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu Gln Xaa Leu Leu Ile Ser
      -15                      -10                      -5

TCC TTG CHA AGA GAG TAC ACA GTC ATT AAT GAA GCH CGC AAG      146
Ser Leu Xaa Arg Glu Tyr Thr Val Ile Asn Glu Ala Arg Lys
      1                      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: 201..266
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.4
 seq FLLCXSVFTDCKG/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```

ACAGAATCAC GTTTTDAGTT GTGCGTGTGC GCGCACACGM GTGTAAAMAG CACTTTCGAT      60

TGTGCCTCCT GTTTTCTCGA GTGGGGACAC TTAACTACA GTTTASACCT CGGGCGCATM      120

AAGTTTKTCT TCTCTTCTC TCTGTTTIT TCTGTTTCTG AGTGGACCAA CAGCAGARCC      180

CACGAGGAKT TGTTTTGAGT ATG GAG CTG TTG CGG GTD TGC TCC TTT TTC TTG      233
      Met Glu Leu Leu Arg Val Cys Ser Phe Phe Leu
      -20                      -15

CTT TGC TSC TCA GTT TTT ACA GAC TGT AAA GGA GAT GTG TTG TGT GTG      281
Leu Cys Xaa Ser Val Phe Thr Asp Cys Lys Gly Asp Val Leu Cys Val
      -10                      -5                      1                      5

```

AAG ATG GAG CAG AGT CAA ATC TGT GCT
 Lys Met Glu Gln Ser Gln Ile Cys Ala
 10

308

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 203..268
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq TWFLLLPPGQCRA/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

AGAATCTCAC GAGAGAAGAA AACCAGCCAC ATAAAGGATT TGAAAGCTCA ACTTGCTTTC 60
 CCACTCTGTT ATCCCTGGAG TTGGCTTGGA TTCACCTGA AGCCTTCCCC CTCCCGGGGA 120
 AAGTTGCTTC ACGTTGCAGC TCAGCAGSTT TGTCCAGCTA CATAGGCTCC AGAAAACAAG 180
 AAGCAAGACT GGAAAGCTGG GG ATG ATT GTA CGC CCT CGC CTG AAT CTT ACG 232
 Met Ile Val Arg Pro Arg Leu Asn Leu Thr
 -20 -15
 TGG TTC CTC CTT CTT CCA CCT GGC CAG TGC AGA GCC GTG GGT GCC ACG 280
 Trp Phe Leu Leu Leu Pro Pro Gly Gln Cys Arg Ala Val Gly Ala Thr
 -10 -5 1
 TGG CCC GGG 289
 Trp Pro Gly
 5

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 1..57
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq MVALCCCLWKISG/CE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```

ATG CAA TTC TTG TTT AAG ATG GTG GCC TTA TGC TGT TGT CTC TGG AAG      48
Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys Leu Trp Lys
          -15                      -10                      -5

ATC TCC GGC TGT GAG GAA GTC CCT CTA ACT TAC AAC CTG CTC AAG TGC      96
Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu Leu Lys Cys
          1                      5                      10

CTC CTA GAT AAA GCG CAC GTA GGG                                      120
Leu Leu Asp Lys Ala His Val Gly
          15                      20

```

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 50..112
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq CVCAAAXXSQLX/XX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```

AAGCGTCCT ATCCGGAGCC AACTGTAGCT GGGATCCAGC GAGAGGAAG ATG CTC AAG      58
                               Met Leu Lys
                               -20

GTG TCA GCC GTA CTG TGT GTG TGT GCA GCC GCT TDG TGS AGT CAG TCT      106
Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Xaa Xaa Ser Gln Ser
          -15                      -10                      -5

CTC GSM RCT KCC GCG GCG GTG GCT GCA GCC GGS GGG CGG TCG GAC GGC      154

```


Leu Xaa Xaa Xaa Ala Ala Val Ala Ala Ala Gly Gly Arg Ser Asp Gly
 1 5 10

GGT AAT TTT CTG GAT GAT AAA CAA TGG CTC ACC ASR ATC TCT CAG TAT 202
 Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu Thr Xaa Ile Ser Gln Tyr
 15 20 25 30

GAC AAG GAA KTC GGM MAG TGG AAC AAA TTC CGA GAC GAT KAT TAT 247
 Asp Lys Glu Xaa Gly Xaa Trp Asn Lys Phe Arg Asp Asp Xaa Tyr
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 124..186
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
 seq MVALCCCLWKISG/CE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

AAGACGCTGC CTTTAGGGAG AGATAAAAAG CATAATGACA TTAGCTAGGA AAGTTAATTT 60

TCAGTTCTTA CTGAAGTGCT GTATGAAACT GAAATTTCCA AGGAACTGAA TTTTGTGAGC 120

CAA ATG AGC ATG CAA TTC TTG TTT AAG ATG GTG GCC TTA TGC TGT TGT 168
 Met Ser Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys
 -20 -15 -10

CTC TGG AAG ATC TCC GGC TGT GAG GAA GTC CCT CTA ACT TAC AAC CTG 216
 Leu Trp Lys Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu
 -5 1 5 10

CTC AAG TGC CTC CTA GAT AAA GCG CAC TGT GTA CTC CTG ACA CCT TGT 264
 Leu Lys Cys Leu Leu Asp Lys Ala His Cys Val Leu Leu Thr Pro Cys
 15 20 25

GGT TAC ATC TTT TCC TTG ATC AGT CCA GGG 294
 Gly Tyr Ile Phe Ser Leu Ile Ser Pro Gly
 30 35

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 114..164
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.2
 seq LWILLGSLSCRTS/NR
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```
AATTCTTATA GGIGTGTCCTA GCAGGCAGTG GCTTGTAGCT GTTCCITCAG CCACTTAACA    60
GGTTTGATTT CAAAGCTTTT TAATAGAGAA ACTAACATGT TTGGAGGGGA TTC ATG      116
                                     Met
GCC CAA CAT TTA TGG ATT TTG TTG GGA AGT CTC AGT TGC CGA ACA AGC      164
Ala Gln His Leu Trp Ile Leu Leu Gly Ser Leu Ser Cys Arg Thr Ser
  -15                      -10                      -5

AAC CGG CGG                                173
Asn Arg Arg
1
```

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 66..149
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.1
 seq LYLFSGFWTFXLG/KF
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

ACACTTGART TGGGGTTAAG TTGAAGAACA GACAACTTA GACACAAAGC TATGCAAAAA   60
TCGTG ATG AAC AAG GAA RAA GTA AGT TTN GAA AGG ARA GCA CAG GTC AGA   110
    Met Asn Lys Glu Xaa Val Ser Xaa Glu Arg Xaa Ala Gln Val Arg
          -25                -20                -15

TTA TAT TTA TTC TCA GGA TTT TGG ACT TTT KTA TTA GGG AAA TTT AAA   158
Leu Tyr Leu Phe Ser Gly Phe Trp Thr Phe Xaa Leu Gly Lys Phe Lys
          -10                -5                1

CAA GGG GAA TGR TCT TAT ATK KGT ATT CTA GAA AGA TTA CTG TGG CAG   206
Gln Gly Glu Xaa Ser Tyr Xaa Xaa Ile Leu Glu Arg Leu Leu Trp Gln
          5                10                15

CAG CAG TAT GWA GGA TGG CTT GTA GGR GAT AAG AGA   242
Gln Gln Tyr Xaa Gly Trp Leu Val Gly Asp Lys Arg
    20                25                30

```

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 200..361
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq IVFIFLILLNTAA/QV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

ATTGAAAGAT GGTAAPATGG TGCAGAAGGG GACTTACACT GAGTTCCTAA AATCTGGTAT   60
AGATTTTGGC TCCCTTTTAA AGAAGGATAA TGAGGAAGT GAACAACCTC CAGTTCCAGG   120
AACTCCACACA MYAAGGGAAT CGTACCCTTC TCAGAGTCTT CGGTTTGGTC TCAACAATCT   180
TCTAGACCCT CCTTGAAAG ATG GTG CTC TGG AGA GCC AAG ATA CAN MGG AAT   232
    Met Val Leu Trp Arg Ala Lys Ile Xaa Arg Asn
          -50                -45

GTC CCA GTT ACA CTA TCA GAG GAG AAC CGT TCT GAA SGA AAA GTT GGT   280
Val Pro Val Thr Leu Ser Glu Glu Asn Arg Ser Glu Gly Lys Val Gly
          -40                -35                -30

TTT CAG GCC TAT AAG AAT TAC TTC AGA GCT GGT GCT CAC TGG ATT GTC   328
Phe Gln Ala Tyr Lys Asn Tyr Phe Arg Ala Gly Ala His Trp Ile Val
    -25                -20                -15

```

```

TTC ATT TTC CTT ATT CTC CTA AAC ACT GCA GCT CAG GTT GCC TAT GTG      376
Phe Ile Phe Leu Ile Leu Leu Asn Thr Ala Ala Gln Val Ala Tyr Val
  -10                      -5                      1                      5

CTT CAA GAT TGG TGG CTT TCA TAC TGG GCA AAC AAA CAA AGT ATG CTA      424
Leu Gln Asp Trp Trp Leu Ser Tyr Trp Ala Asn Lys Gln Ser Met Leu
          10                      15                      20

AAT GTC ACT GTA AAT                                          439
Asn Val Thr Val Asn
          25

```

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 125..178
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq FTSVLWLTSPSQP/NT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

ATGTAGTGAA TAAAGTTTGA GAACCACTGA CTTGAACTTT AGCATGATTT GATACACAGG      60
GTCCCTCTGTA ATCGTACTTC GTTCTGCTTT AAGGCTGTTG GGCTGTCTCC TCCAACCCAT      120
CCKK ATG TTG TTG TAK TTT TTC ACC TCK GTC CTT TGG CTT ACG TCA CCN      169
Met Leu Leu Xaa Phe Phe Thr Ser Val Leu Trp Leu Thr Ser Pro
          -15                      -10                      -5

TCC CAA CCT AAT ACC TGC CCT TCT AGT CTT CTG TGT ACT TAT CCA AAT      217
Ser Gln Pro Asn Thr Cys Pro Ser Ser Leu Leu Cys Thr Tyr Pro Asn
          1                      5                      10

CTA AAC CCT CCA TGG                                          232
Leu Asn Pro Pro Trp
          15

```

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 140..205
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq IILGCLALFLLQ/RK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```
AACAGTTACG AAGGAGAGCT GCAAAAGITG CAGCAGAAAG GTTGGGAGTC CCGACAGGTT    60
CCGTAGCCCA CAGAAAAGAA GCAAGGGACG GCAGGACTGT TTCACAGTTT TCTGCTTCTG    120
GAAGGTGCTG GACAAAAAC ATG GAA CTA ATT TCC CCA ACA GTG ATT ATA ATC    172
              Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile
              -20                               -15

CTG GGT TGC CTT GCT CTG TTC TTA CTC CTT CAG CGG AAG AAT TTG CGC    220
Leu Gly Cys Leu Ala Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg
-10                               -5                               1                               5

AGA CCC TGG    229
Arg Pro Trp
```

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 134..274
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq TWLGLLSFQNLHC/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

```

ATCATTTTCT TATCCCTGCT GATTTCAAAC CTCGCCATGG TTAGAAACA TAACTGTAA      60
TGTAAATGCAA GTCCCTAAC TCCCTGGTTG CTAACATTAA CTTCCTTAAG TAATAATCAA    120
TGAAAGAVAT TCT ATG CAT GST TTT GAA ATA ATA TCC TTT AAA GAG GAA      169
      Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu
      -45                               -40

TCA CCA TTA CGA AAG GTG AGT CAG GGT CCT TTG TTT AAT GTG ACT AGT      217
Ser Pro Leu Gly Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser
-35                               -30                               -25                               -20

GGC TCA TCA TCA CCA GTG ACC TGG TTG GGC CTA CTC TCC TTC CAG AAC      265
Gly Ser Ser Ser Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn
      -15                               -10                               -5

CTG CAT TGC TTC CCA GAC CTC CCC GGG                                  292
Leu His Cys Phe Pro Asp Leu Pro Gly
      1                               5

```

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 270..437
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq NTLFLHLSGLSAA/DT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

```

AAGCTCTGAG ACAGGAGCCC AGCCCTGGGA TTTTCAGGTG TTTTCATTTG GTGGTCAGGC      60
CTGAACAGAG TGTTTTCTTT TGGTGGTCAG GACTGAGCAG AGAGACCTCA CCATGGAGCT    120
TKGGSYGKTG CKGGCTTTTT CTGTGGCCA TTTTGAAAGA TGTCGGGTCT GAGGGACAAC    180
TATTGGAATC TGGGGGAAGT TCGGTCCAGC CCGGGGAGTC CCTGGGACTC TCCTGTGCAG    240
CCGCTGGATT CGCNTTTCGC AATTTTSCC ATG ACT TGG GTC CGC CAC GCT CCA      293
      Met Thr Trp Val Arg His Ala Pro
      -55                               -50

GGG AAG AGT CTG GAA TGG GTC GCA ACC GTC ACA GAT GGT GST GAT AAG      341
Gly Lys Ser Leu Glu Trp Val Ala Thr Val Thr Asp Gly Gly Asp Lys
      -45                               -40                               -35

```

```

ACC TTT TAT GCG GCC TCC GTG AAG GGC CGC TTC AAC CTC TCC AGG GAC    389
Thr Phe Tyr Ala Ala Ser Val Lys Gly Arg Phe Asn Val Ser Arg Asp
      -30                -25                -20

AAT TCC AAG AAC ACG TTA TTT CTG CAT TTG AGC GGC CTG AGT GCC GGC    437
Asn Ser Lys Asn Thr Leu Phe Leu His Leu Ser Gly Leu Ser Ala Ala
      -15                -10                -5

GAC ACC GGC TGG TGG GGG ATC    458
Asp Thr Gly Trp Trp Gly Ile
      1                5

```

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 143..184
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq LTSFFSLTANCQS/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

```

AACATACCCT TCAGGTTTAG GTCTTTCTTA GGTAAAGTTT TAACTTTAGT ATATCTTCCT    60
CAGGGCGGCC TTCTCCTTCC CCCTAGTAAG TGRAGAAACC CTTGTGKTG TGCCCTCTGA    120
ACTCACCGCA TTTGGGATTA CC ATG CTA ACA TCC TTT TTT TCA CTG ACT GCA    172
                Met Leu Thr Ser Phe Phe Ser Leu Thr Ala
                        -10                -5

AAT TGC CAG AGT GCA GGA ACT ATC TCA TTT GCT GCT TTC TCC CTA ATG    220
Asn Cys Gln Ser Ala Gly Thr Ile Ser Phe Ala Ala Phe Ser Leu Met
      1                5                10

CCT GGA    226
Pro Gly

```

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 72..125
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.8
seq LTPLFFMXPTGFS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

ACTTCCCTTC CCCCTCTAGC ATTGCTACCT TCTCTCCTAC ACGCACGCAG SCATATAAAC    60
GTAGGTITTT G ATG CTC CTC TGC CTG TTG ACC CCG CTA TTT TTC ATG TTK    110
               Met Leu Leu Cys Leu Leu Thr Pro Leu Phe Phe Met Xaa
               -15                               -10

CCA ACA GGT TTT TCT TCC CCC AGT CCT GGG                                140
Pro Thr Gly Phe Ser Ser Pro Ser Pro Gly
-5                               1                               5

```

(2) INFORMATION FOR SEQ ID NO: 100:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 178..240
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq HSLFLSLLGLCPS/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```

AATGGCGCG GGGCGTCCGT AGCCACGGCA ACAGGTGCT TGTGAGTCT GAGCTGAGCG    60
CCTTTCGCAC GACTTGGAGT TACGGTTTAT TTGATACCCC GGTACCCCTA CGCAAGCAAG    120
CCCACATCGA CACACATTCA CACACGCCCT TCAGCACCCC CTCCCAGCAC CACGACC      177

```


G TTC TTG TCG CTC CTC 225
 u Phe Leu Ser Leu Leu
 -10

A AAT GGT CCC GTC TTT 273
 u Asn Ala Pro Val Phe
 10

288

prostate

Heijne matrix
 5.7
 VWLLLGHMVVS/QM

0: 101:

CG TCCCAATTAT ACCCGGTTGG 60

LA AATCTTCGTA CCCATTTTGC 120

CC TCGTGCCAA GGAGCCATGC 180

CT AGGCTTCAC TTCTATTCCT 240

CT TTGAGTGGAG CTTCTGG 297

CT CTC CTT GGC CAC ATG 345

u Leu Leu Gly His Met
 -5

CA AAG CAC AGA CCC TGG 393

rg Lys His Arg Pro Trp
 10

- (A) LENGTH: 281 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 135..251
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq LTQGVWLWLVQA/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```

ATATACAGAG AATAACGTC ATCCCTCTAA CATTAAATATG TTCAGTTTTA TGTACCTGAG    60
AGTTGATGGT TTAATTTGTG GGTGTTGCCA GACTCTCTTG CGACTTCTCT CATCATCTGC   120
TCTTTAGCAC TTCC ATG AGA CGG GGC AAG AGA TTG TTG GAG TCT CAA TCC       170
      Met Arg Arg Gly Lys Arg Leu Leu Glu Ser Gln Ser
                        -35                               -30

AGC AGC CCG AAA GCC TGT CTG CAG CTT GGG TTT GAG ACT GAA CTA ACT       218
Ser Ser Pro Lys Ala Cys Leu Gln Leu Gly Phe Glu Thr Glu Leu Thr
      -25                               -20                               -15

CAG GGT GTT TTG TGG ATT TTA GTT ATC CAG GCT GTC CCT GTT CCC TCA       266
Gln Gly Val Leu Trp Ile Leu Val Ile Gln Ala Val Pro Val Pro Ser
      -10                               -5                               1                               5

TTA ACA AAA ACA AAA                                                    281
Leu Thr Lys Thr Lys
                        10

```

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 205..264
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7
seq ALLESVVWLPCHG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

AGACCAGGCG CATTTCCTCAG AAGCCTTTGG CTCCCCTGAG ATGCCAAATA GCGGCTCACT    60
CTTCCGCCTC CACGSACTGG CTTTGSTGTT CATGCTGCTT GGGATGTCTA CTATGGACCT    120
GCTGAGCACA GGCCTGGCTT CCTGGGGCAC AGAGTTGATG CTTATGGCCC AGGAACIGCT    180
GGGCCCCAGG ACTGGGCGGT TTCC ATG GTT GCT GCC ACA GAA GCA GCA TTG    231
                        Met Val Ala Ala Thr Glu Ala Ala Leu
                        -20                      -15

CTG GAG TCA GTA GTG TGG CTG CCT TGC CAT GGC CGT GGT GGG TCT    276
Leu Glu Ser Val Val Trp Leu Pro Cys His Gly Arg Gly Gly Ser
-10                      -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 356..412
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq VSLPLLSSWGSTA/WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

AATTACAGCT CTACAATGCA CCAGACGGAC CCATCTGGAT TCTTTCGGGG CTCTTAGCCC    60
TAGAAATAGC ATCATTTCCT CAAACTGGTG AGTCCTCCTG TCTAAAATCA GGATGCAGAG    120
AGTTGATGCA CGGCATGGCA CAGGATGCTG GGCAAGGCTG GCAGGCCCGG GAGAGCCTGT    180
GGCCAGCCTG GGTCCAGGAA GTGGGCAGCT GCCACAGAGG GGCCTCCGAG GCTAGCTGCC    240
TCCTAACTTC CTCACGGCAC ACCATTCTGC CGTCCTGAGT CTTCTCAAGG TTGGAAGGTG    300
CCCAGATCCA GGGAGATGGT GCTGGCTCTT TGGTGGCTGT GGAGTGTCCA GACAG ATG    358
                        Met

AGC TGG AAT CCT TCA GTT TCT CTG CCT CTC CTG TCA AGT TGG GGT AGC    406
Ser Trp Asn Pro Ser Val Ser Leu Pro Leu Leu Ser Ser Trp Gly Ser

```

- 15

-10

-5

ACT GCT TGG ACT CTT
Thr Ala Trp Thr Leu
1

421

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: 53..118
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
 seq LILLSLHLERRWT/SP
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

ACAATAATAA CTAATGAGAT TAAAAATTAA AACAGGTGTC TGATAATCCT TG ATG AAG 58  
Met Lys

AGA ATT CAG GGG ATA TTG TTC CTG ATT TTG CTT TCT CTC CAC TTG GAA 106  
Arg Ile Gln Gly Ile Leu Phe Leu Ile Leu Leu Ser Leu His Leu Glu  
-20 -15 -10 -5

AGG AGG TGG ACG AGC CCA TCA GAC CAC AGC CTG TTG CTA GGA GGA AAT     154  
Arg Arg Trp Thr Ser Pro Ser Asp His Ser Leu Leu Leu Gly Gly Asn

                1                              5                            10

TCC TTG GCT CAA CAT GCA GAA AGT GTA GTA CGC CAA GGG 193  
Ser Leu Ala Gln His Ala Glu Ser Val Val Arg Gln Gly  
15 20 25

(2) INFORMATION FOR SEQ ID NO: 106:

## (2) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(21) MOLECULE TYPE: CDNA

(v<sub>1</sub>) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 298..402  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.5  
 seq LLTFGLEVCLAAG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```

AAAGGAAGGG GGGGCGGAAC CAGCCTGCAC GCGCTGGCTC CGGGTGACAG CCGCGCGCCT 60
CGGCCAGGAT CTGAGTGATG AGACGTGTCC CCACTGAGGT GCCCCACAGC AGCAGGTGTT 120
GAGCATGGGC TGAGAAGCTG GACCGGCACC AAAGGGCTGG CAGAAATDVG CGCCTGGCTG 180
ATTCCTAGGC AGTTGGCRGC AGCAAGGAGG AGAGGCCGCA GCTTCTGGAG CAGAGCCGAG 240
ACGAAGCAGT TCTGGAGTGC CTGAACGGCC CCCTGAGCCC TACCGGCCTG GCCCACT 297
ATG GTC CAG AGG CTG TGG GTG AGC CGC CTG CTG CGG CAC CGG AAA GCC 345
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
-35 -30 -25 -20
CAG CTC KKG CTG GKC AAC CTG CTA ACC TTT GGC CTG GAG GTG TGT TTG 393
Gln Leu Xaa Leu Xaa Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
-15 -10 -5
GCC GCA GGA TCA CCT ATG TGC CGC CTC TGC TGC TGG AAG TGG 435
Ala Ala Gly Ser Pro Met Cys Arg Leu Cys Cys Trp Lys Trp
1 5 10

```

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 27..80  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.5  
 seq PFALVTSCSSVFS/GD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```

AGACGGAACC AGCTCGCGAG CGCACT ATG GCT GCT GGC GTA CCC TTT GCG TTA 53

```

```

Met Ala Ala Gly Val Pro Phe Ala Leu
-15 -10

GTC ACC AGC TGC TCC TCC GTC TTC TCA GGA GAC CAG CTG GTC CAA CAT 101
Val Thr Ser Cys Ser Ser Val Phe Ser Gly Asp Gln Leu Val Gln His
-5 1 5

ATC CTT GGA ACA GAA GAT CTT ATT GTG GAA GTG ACT TCT AAT GAT GCT 149
Ile Leu Gly Thr Glu Asp Leu Ile Val Glu Val Thr Ser Asn Asp Ala
10 15 20

GTG AGA TTT TAT CCC TGG ACC ATT GAT AAT AAA TAC TAT TCA GCA GAC 197
Val Arg Phe Tyr Pro Trp Thr Ile Asp Asn Lys Tyr Tyr Ser Ala Asp
25 30 35

ATC AAT CTA TGT GTG GTG CCW AAC AAA TTT CTT GTT ACT GCA GAG ATT 245
Ile Asn Leu Cys Val Val Pro Asn Lys Phe Leu Val Thr Ala Glu Ile
40 45 50 55

GCA GAA TCT GTC CAA GCA TTT GTG GTT TAC TTT GAC DKC ACA CAA RAA 293
Ala Glu Ser Val Gln Ala Phe Val Val Tyr Phe Asp Xaa Thr Gln Xaa
60 65 70

TCG GGC CTT GAT AGT GTC TCC TCA TGG CTT CCA CTG GCA AAA GCA TGG 341
Ser Gly Leu Asp Ser Val Ser Ser Trp Leu Pro Leu Ala Lys Ala Trp
75 80 85

TTA CCT GAG GTG ATG ATC TTG GTC TGC GAT AGA GTG TCT GAA GAT GGT 389
Leu Pro Glu Val Met Ile Leu Val Cys Asp Arg Val Ser Glu Asp Gly
90 95 100

ATA 392
Ile

```

## (2) INFORMATION FOR SEQ ID NO: 108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 290..331
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq TVFLXFCFPRCHS/DS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

AATGCTGAAC GGWCACACAG AGAGGAAACW ATAAATKKYA GCTACTATGC AATAAATATC 60

```

TCAGGTTTTA ACGAAGAAAA ACATCATTGC AGTGAAATAA AAAATTTTAA AATTTTAGAA 120
CAAAGCTAAC AAATGGCTAG TTTTCTATGN TTCTTCTTCA AACGCTTTCT TTGAGGGGRM 180
AAGAGTCAMA CAAACAAGCA GTTTTACCTA AAATAAAGAA CTAGTTTTAG AGGTCAGAMG 240
AMAGSMGCAA GTTTTGCGAG WGGCACGGAA GGAGTGTGCT GGCAGTACA ATG ACA GTT 298
 Met Thr Val
TTC CTT TMN TTT TGC TTT CCT CGC TGC CAT TCT GAC TCA CAT ARG RTG 346
Phe Leu Xaa Phe Cys Phe Pro Arg Cys His Ser Asp Ser His Xaa Xaa
-10 -5 1 5
CAG CAA TCA GCG 358
Gln Gln Ser Ala

```

## (2) INFORMATION FOR SEQ ID NO: 109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 44..187
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq ILLEVFVWNLQG/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

```

AASTTCTTCC TGCCAAGAGA ACAATGCCGA GAAACAGAGC GAA ATG KTT CCA AAT 55
 Met Xaa Pro Asn
 -45
AAT TTT TGG CAA AAA CTT GGA AGA AAA AAA CCC CGC ATA TTT ACC TGT 103
Asn Phe Trp Gln Lys Leu Gly Arg Lys Lys Pro Arg Ile Phe Thr Cys
-40 -35 -30
ACC CAG AGC TCC ACA GGT GAG GCG GCA GTT AAA GCA GAA AAT CTA ATT 151
Thr Gln Ser Ser Thr Gly Glu Ala Ala Val Lys Ala Glu Asn Leu Ile
-25 -20 -15
CTT CTG GAA GTT TTT GTC TGG AAC GGA CTC CAG GGT CTT CCT TCG GAG 199
Leu Leu Glu Val Phe Val Trp Asn Gly Leu Gln Gly Leu Pro Ser Glu
-10 -5 1
CTG TCA GAT ACA AGT GGA TCC TCT AAG AAA CTT GGG AGC CTT GTG GGC 247
Leu Ser Asp Thr Ser Gly Ser Ser Lys Lys Leu Gly Ser Leu Val Gly

```

|                                                                 |     |    |    |  |
|-----------------------------------------------------------------|-----|----|----|--|
| 5                                                               | 10  | 15 | 20 |  |
| TGG TGG AGA ACT CTC AAG ATG GCA CCA GCC TGT CTA TGG TCT ATG TGG | 295 |    |    |  |
| Trp Trp Arg Thr Leu Lys Met Ala Pro Ala Cys Leu Trp Ser Met Trp |     |    |    |  |
| 25 30 35                                                        |     |    |    |  |
| GAA TCA CCG CCA CGG                                             | 310 |    |    |  |
| Glu Ser Pro Pro Arg                                             |     |    |    |  |
| 40                                                              |     |    |    |  |

## (2) INFORMATION FOR SEQ ID NO: 110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 66..173
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq ALYIMCVPHSVWG/CA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAGTCCAGAG GCCTGGCCCT GCCAAGAAGG CGCTCTCCGG AATCAACACC TGGGGGCTTG | 60  |
| GAAGG ATG TTT CGC TCA GAT CGA ATG TGG ARC TGC CAT TGG AAA TGG AAG | 110 |
| Met Phe Arg Ser Asp Arg Met Trp Xaa Cys His Trp Lys Trp Lys       |     |
| -35 -30 -25                                                       |     |
| CCC AGT CCT CTC CTG TTC TTA TTT GCT TTA TAT ATC ATG TGT GTT CCT   | 158 |
| Pro Ser Pro Leu Leu Phe Leu Phe Ala Leu Tyr Ile Met Cys Val Pro   |     |
| -20 -15 -10                                                       |     |
| CAC TCA GTG TGG GGA TGT GCC AAC TGC CGA GTG GTT TTG TCC AAC CCT   | 206 |
| His Ser Val Trp Gly Cys Ala Asn Cys Arg Val Val Leu Ser Asn Pro   |     |
| -5 1 5 10                                                         |     |
| TCT GGG ACC TTT ACT TCT CCA TGC TAC CCT AAC GAC TAC CCA AAC AGC   | 254 |
| Ser Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser   |     |
| 15 20 25                                                          |     |
| CAG GCT TGC ATG TGG ACG CTC CGA GAC CCC                           | 284 |
| Gln Ala Cys Met Trp Thr Leu Arg Asp Pro                           |     |
| 30 35                                                             |     |

## (2) INFORMATION FOR SEQ ID NO: 111:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 398 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 123..215  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.3  
 seq LVALSSELPLGA/GV
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

TCCTTCATCT TGTGTTCTAA AACCTTGCAA GTTCAGGAAG AAACCATCTG CATCCATATT 60
GAAAACCTGA CACAATGTAT GCAGCAGGCT CAGTGTGAGT GAACTGGAGG CTTCTCTACA 120
AC ATG ACC CAA AGG AGC ATT GCA GGT CCT ATT TGC AAC CTG AAG TTT 167
 Met Thr Gln Arg Ser Ile Ala Gly Pro Ile Cys Asn Leu Lys Phe
 -30 -25 -20

GTG ACT CTC CTG GTT GCC TTA AGT TCA GAA CTC CCA TTC CTG GGA GCT 215
Val Thr Leu Leu Val Ala Leu Ser Ser Glu Leu Pro Phe Leu Gly Ala
 -15 -10 -5

GGA GTA CAG CTT CAA GAC AAT GGG TAT AAT GGA TTG CTC ATT GCA ATT 263
Gly Val Gln Leu Gln Asp Asn Gly Tyr Asn Gly Leu Leu Ile Ala Ile
 1 5 10 15

AAT CCT CAG GTA CCT GAG AAT CAG AAC CTC ATC TCA AAC ATT AAG GAA 311
Asn Pro Gln Val Pro Glu Asn Gln Asn Leu Ile Ser Asn Ile Lys Glu
 - 20 25 30

ATG ATA ACT GAA GCT TCA TTT TAC CTA TTT AAT GCT ACC AAG AGA AGA 359
Met Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala Thr Lys Arg Arg
 35 40 45

GTA TTT TTC AGA AAT ATA AAG ATT TTA ATA CCT GCC CAG 398
Val Phe Phe Arg Asn Ile Lys Ile Leu Ile Pro Ala Gln
 50 55 60

```

(2) INFORMATION FOR SEQ ID NO: 112:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 187..228  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.3  
seq IIPLLLLLRSACN/VH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```

ACTCCAGGAG CCGGGACCAA AATAACCGGG CGGGAGGGGA CACCTCGCAG AGATGGATCT 60
CGAACTCCTG GGCTCAAGCG ATCCTTTCAC CTTGGCCTCT CAAGTAGCTG GGACCACATT 120
TGCTCACCAG CTGGCCCAAG ACCAGACTGG GCAACATGGG TCATCCTCCT CTAAGATTCC 180
AGGACC ATG ATC ATC CCT CTA TTG CTA CTT CTT AGA TCA GCT TGT AAT 228
 Met Ile Ile Pro Leu Leu Leu Leu Arg Ser Ala Cys Asn
 -10 -5

GTC CAT CTC CCC CAC CAG ACT GCG TCT CCA GCA TCT CTG AGT CCC CAG 276
Val His Leu Pro His Gln Thr Ala Ser Pro Ala Ser Leu Ser Pro Gln
 1 5 10 15

GGC CTG GCC TGG GGC TTG CTA CAT GCT GGG TGC TCA GTA ACT GTG AGA 324
Gly Leu Ala Trp Gly Leu Leu His Gly Gly Cys Ser Val Thr Val Arg
 20 25 30

```

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 231..287  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.3  
seq VLLLSXNLNLIQ/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```

ACTATGGAGG GAAGACACAG GGAAAGGAGT ATTTCAAAAA CTTTAAATAA TTGTACATAA 60

```

TTGGAGCAAG TGAGAAGACA AGTKAGAGGT AAGCWGKTRT TGAGAATAGG GKKCTGATTG 120  
 TGCCAGCTTT GTATACVATT ATNAGGAACN DGGACTTTGT CCTGAAGGTA ACTGGGCAAT 180  
 TGTGAGGTC ACCACCATCT ACTGTCTGGA TTAACGAGGA AACTTTCTAA ATG TMS 236  
 Met Xaa  
 TCT CCA CTT CCA GTC CTG CTC CTC TCA TGC AAT CTC AAC CTA ATA ATT 284  
 Ser Pro Leu Pro Val Leu Leu Leu Ser Xaa Asn Leu Asn Leu Ile Ile  
 -15 -10 -5  
 CAG AGT AGT 293  
 Gln Ser Ser  
 1

## (2) INFORMATION FOR SEQ ID NO: 114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 244..381
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq LLTFLVFTXKLSS/LN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

ACACTGAAAT CAATCTGTTC AATAGCAITTA TACCATATTT GACATACCAT AGCCATGTTA 60  
 ATCTGATATT GTAGAATAGC ATAGTAKAAT AATAATAACT CCTAACTCAA GGATGTTGWG 120  
 WKCCTTTATA ACCAGCAATC CATGTTARAT ATTAGCACAG TGCCTAAAAC ATATTAAGCA 180  
 TTCAATAAAT GATCGCTACT ATTTTACTA ACATCCTACA GATTTGGAAA TTGACTCTTA 240  
 GAA ATG TTA ATG TGT AAA ATG CTA AAG AGC CAA AAA AAC TGC CAG GAA 288  
 Met Leu Met Cys Lys Met Leu Lys Ser Gln Lys Asn Cys Gln Glu  
 -45 -40 -35  
 AAT ATR ARA ATT AAA ATC ATT TTA TTT CTG AAA CCC ATG TGT TCC CCC 336  
 Asn Xaa Xaa Ile Lys Ile Ile Leu Phe Leu Lys Pro Met Cys Ser Pro  
 -30 -25 -20  
 CAA TAT CTT CTA ACA TTT CTA GTA TTT ACA GRA AAA CTT TCA AGT CTC 384  
 Gln Tyr Leu Leu Thr Phe Leu Val Phe Thr Xaa Lys Leu Ser Ser Leu  
 -15 -10 -5 1

AAT AIC RGA AAG TTT CAT  
 Asn Ile Xaa Lys Phe His  
 5

402

## (2) INFORMATION FOR SEQ ID NO: 115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 306..461
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq IIVILHCAASIIS/CP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

AAGTATTAAA TTAAAAAGA TAAATCTGCC CTATTCTAAT CATGTCTTG TCTTCTGTTT 60
ATTCAAGTGT ATTCCATTG CTTTCGGGAA TATTTGGATG TTTTAGAACT AACATTCTGC 120
TTTAATAATC CAAACACRCK AYMAYTYCCA TCAATTTGAG TCTCTTAAAA TGTTACACTG 180
AAATGAATCT CTCTGAAGAT GGAATTATTG ATTTCTATAT TCTTCCTCTA GCATCATGAA 240
ATTTGACCTC TTCAGCCGTG CATGGTTAAC ACTCAGATAA CCCATCTCCT TGAGAAGAAC 300
CCCTG ATG AAR AAG AAA TCC TCT CCA AAT CAA TAT CTT CAT TCA TCA CTA 350
 Met Lys Lys Lys Ser Ser Pro Asn Gln Tyr Leu His Ser Ser Leu
 -50 -45 -40

CAC TRS ATA CGN CTA TTT TCC TTC CTC CAT TTC TCA GAG GAA GGA GTT 398
His Xaa Ile Arg Leu Phe Ser Phe Leu His Phe Ser Glu Glu Gly Val
 -35 -30 -25

CTA TTA CTT GCC ATT GAT CTT AAA ATT ATA GTT ATC CTC CAC TGT GCT 446
Leu Leu Leu Ala Ile Asp Leu Lys Ile Ile Val Ile Leu His Cys Ala
 -20 -15 -10

GCA TCC ATA ATT TCA TGT CCC TCA 470
Ala Ser Ile Ile Ser Cys Pro Ser
 -5 1

```

## (2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 334 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Prostate
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 116..184  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.1  
 seq ATSVSLEAQSCFA/WP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

ATTTTGGAAA ACTGTAATGC TTTAAACTT ACTTTATTGG ATCTCTTTCG AGCTTTTGAC 60
ACASTGAACC ACTTTCCTTT CCTGAAATGC TTTCCTCTCT TGGCTTTCCTG ATGCC ATG 118
 Met
TTC TCC TGT TTC TTC TCT ACT TCT CTG GCC ACT TCT GTC TCC TTA GAA 166
Phe Ser Cys Phe Phe Ser Thr Ser Leu Ala Thr Ser Val Ser Leu Glu
 -20 -15 -10

GCT CAG TCT TGC TTT GCC TGG CCC TTG ATT GTT AGT TTT CCC CAG GGC 214
Ala Gln Ser Cys Phe Ala Trp Pro Leu Ile Val Ser Phe Pro Gln Gly
 -5 1 5 10

TCA CTT CTT AGC CCC TTT CTC CTC ATG TCT TAT AAT TTG AGT CAT CTC 262
Ser Leu Leu Ser Pro Phe Leu Leu Met Ser Tyr Asn Leu Ser His Leu
 15 20 25

ATC TAC TCT GGG GAG TTG AAT GGT CGC TTG TAT GCT GAA AAC TCC CAA 310
Ile Tyr Ser Gly Glu Leu Asn Gly Arg Leu Tyr Ala Glu Asn Ser Gln
 30 35 40

ATT TGT ATC TGT AGC CCA GCC GGG 334
Ile Cys Ile Cys Ser Pro Ala Gly
 45 50

```

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 302 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 78..227  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.1  
 seq RTALILAVQKSSA/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```

AGTTTCCAAG GGAAGGAGCA GCGTGTGGGA AAGCACAGAA GAGTGAGAAG GAAGCGACTA 60
AATTTTATTT ACTTTCT ATG CAT CAT GGC CTC ACA CCA CTG TTA CTT GGT 110
 Met His His Gly Leu Thr Pro Leu Leu Leu Gly
 -50 -45 -40

GTA CAT GAG CAA AAA CAG CAA GTG GTG AAA TTT TTA ATC AAG AAA AAA 158
Val His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys
 -35 -30 -25

GCA AAT TTA AAT GCA CTG GAT AGA TAT GGA AGA ACT SCT CTC ATA CTT 206
Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu
 -20 -15 -10

GCT GTA TGT TGT GGA TCG GCA AGT ATA GTC AGC CTT CTA CTT GAG CAA 254
Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln
 -5 1 5

AAC ATT GAT GTA TCT TCT CAA GAT CTA TCT GGA CAG ACG GCC CCC GGG 302
Asn Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Pro Gly
 10 15 20 25

```

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 319..369  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.1  
 seq IYFFACFQALTSS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

```

AGAGTAGGCG GAGACAGAGA GGCTGTATTT CAGTGCAGCC TGCCAGACCT CTTCTGGAGC 60

```

```

AASACTGGAC AAAGGGGGTC ACACATTCCT TCCATACGGT TGAGCCTCTA CCGGCTGGT 120
GCTGGTCACA GTTCAGCTTC TTCATGATGG TGGATCCCAA TGGJAATGAA TCCAGTGCTA 180
CATACTTCAT CCTAATAGGC CTCCTGGTT TAGAAGAGGG TCAATCTGG TTGGCCTTCC 240
CAATGTGCTC CCTCTACCTT ATTGCTGTGC TAGGTAACCT GACAATCATC TACATTGTGC 300
GGAATGAGCA CAGCCTGC ATG AGC CCA TGT ATA TAT TTC TTT GCA TGC TTT 351
Met Ser Pro Cys Ile Tyr Phe Phe Ala Cys Phe
-15 -10

CAG GCA TTG ACA TCC TCA TCT CCA CCT CAG 381
Gln Ala Leu Thr Ser Ser Ser Pro Pro Gln
-5 1

```

## (2) INFORMATION FOR SEQ ID NO: 119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 49..141
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq VSGASGFLPPARS/RI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```

CTTTCTGTGT CTCCTTCCT CCGCCTCAGT TTGGGGCGGG TCGGGGGA ATG GCT GAG 57
Met Ala Glu
-30

GAG ATG GAG TCG TCG CTC GAG GCA AGS TTT TCG TCC AGC GGG GCA CTC 105
Glu Met Glu Ser Ser Leu Glu Ala Xaa Phe Ser Ser Ser Gly Ala Val
-25 -20 -15

TCA GGG GCC TCA GGG TTT TTG CCT CCT GCC CGC TCC CGC ATC TTC AAG 153
Ser Gly Ala Ser Gly Phe Leu Pro Pro Ala Arg Ser Arg Ile Phe Lys
-10 -5 1

ATA ATC GTG ATC GGC GAC VBC AAT GTG GGC AAG ACA TGC CTG ACC TAC 201
Ile Ile Val Ile Gly Asp Xaa Asn Val Gly Lys Thr Cys Leu Thr Tyr
5 10 15 20

CGC TTC TGC GCT GGC CGC TTC CCC GAC CGC ACC GAG GCC ACG ATA GGT 249
Arg Phe Cys Ala Gly Arg Phe Pro Asp Arg Thr Glu Ala Thr Ile Gly

```

|                                                                 |    |    |     |
|-----------------------------------------------------------------|----|----|-----|
| 25                                                              | 30 | 35 |     |
| GTG GAT TTC CGA GAA CGA GCG GTG GAG ATT GAT GGG GAG CGC ATC AAG |    |    | 297 |
| Val Asp Phe Arg Glu Arg Ala Val Glu Ile Asp Gly Glu Arg Ile Lys |    |    |     |
| 40                                                              | 45 | 50 |     |
| ATC CAG CTA TGG GAC ACA GCA                                     |    |    | 318 |
| Ile Gln Leu Trp Asp Thr Ala                                     |    |    |     |
| 55                                                              |    |    |     |

## (2) INFORMATION FOR SEQ ID NO: 120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 61..153
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq VSGASGFLPPARS/RI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

|                                                                             |     |
|-----------------------------------------------------------------------------|-----|
| AAATCTCTCA GCCTTTCTGT GTCTCCTTTC CTCCGCCTCA GTTGGGGGCG GGTGGGGGGA           | 60  |
| ATG GCT GAG GAG ATG GAG TCG TCG CTC GAG GCA AGC TTT TCG TCC AGC             | 108 |
| Met Ala Glu Glu Met Glu Ser Ser Leu Glu Ala Ser Phe Ser Ser Ser             |     |
| -30                      -25                      -20                       |     |
| GGG GCA GTG TCA GGG GCC TCA GGG TTT TTG CCT CCT GCC CGC TCC CGC             | 156 |
| Gly Ala Val Ser Gly Ala Ser Gly Phe Leu Pro Pro Ala Arg Ser Arg             |     |
| -15                      -10                      -5                      1 |     |
| ATC TTC AAG ATA ATC GTG ATC GGC GAC TCC AAT GTD VGC AAG ACA TGC             | 204 |
| Ile Phe Lys Ile Ile Val Ile Gly Asp Ser Asn Val Xaa Lys Thr Cys             |     |
| 5                      10                      15                           |     |
| CTG ACC TAC CGC TTC TGC GCT GGC CGC TTC CCC GAC CGG                         | 243 |
| Leu Thr Tyr Arg Phe Cys Ala Gly Arg Phe Pro Asp Arg                         |     |
| 20                      25                      30                          |     |

## (2) INFORMATION FOR SEQ ID NO: 121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: NUCLEIC ACID



(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 153..233  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5  
seq HLSLILLKPLCLP/NN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

```

ACCTTTTATA AACATTTTGT TTAACTTTTA TTGTGGTAAA ATACACATAA CACTTCTCTT 60
CTTTTAGACC TGGGCTGGTA AGAAGTGCTG AAGATGTTTT TTAGAGATTG GTGGTATGAC 120
AAATTCCACT GGGGTTTCTG ASCTTCTCAG TC ATG CTT GTC TTG GGG TCA CCA 173
 Met Leu Val Leu Gly Ser Pro
 -25

CTC CTT GGC CCT CTC CTA TGG CAC CTG TCC CTC ATT CTG CTC AAG CCC 221
Leu Leu Gly Pro Leu Leu Trp His Leu Ser Leu Ile Leu Leu Lys Pro
-20 -15 -10 -5

CTA TGC CTT CCC AAC AAC TTG CCT TTA GCT CTG GGC AGA TGT CTT TGC 269
Leu Cys Leu Pro Asn Asn Leu Pro Leu Ala Leu Gly Arg Cys Leu Cys
 1 5 10

TTG CAC TCG 278
Leu His Ser
15

```

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 56..220  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5  
seq VLFMTTAVDLVIT/EV

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```

AGAAAGGTGT TTTGGTCTTC TCCTTAGTCC AGGAAAAGAT GTACGAAATA GTGAC ATG 58
 Met
 -55

CAC TTA TTA GAT TTG GAA TCT ATG GGC AAA AGT TCA GAT GGA AAG TCG 106
His Leu Leu Asp Leu Glu Ser Met Gly Lys Ser Ser Asp Gly Lys Ser
 -50 -45 -40

TAT GTT ATT ACG GGG AGC TGG AAT CCA AAA TCC CCA CAT TTT CAA GTT 154
Tyr Val Ile Thr Gly Ser Trp Asn Pro Lys Ser Pro His Phe Gln Val
 -35 -30 -25

GTA AAT GAA GAA ACT CCT AAA GAT AAA GTC CTG TTT ATG ACC ACA GCT 202
Val Asn Glu Glu Thr Pro Lys Asp Lys Val Leu Phe Met Thr Thr Ala
 -20 -15 -10

GTA GAT TTG GTA ATA ACA GAA GTA CAG GAG CCT GTT CGA TTT CTC CTG 250
Val Asp Leu Val Ile Thr Glu Val Gln Glu Pro Val Arg Phe Leu Leu
 -5 1 5 10

GAG ACA AAA GTC CGC GTT TGC TCA CCT AAT GAA AGA TTA TTC TGG CCC 298
Glu Thr Lys Val Arg Val Cys Ser Pro Asn Glu Arg Leu Phe Trp Pro
 15 20 25

GCG
Ala
 301

```

## (2) INFORMATION FOR SEQ ID NO: 123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1..63
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq VLFVFSSIPTFL/FQ

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

ATG GAG AAT TTG AAA GAC TTT TAT GTG TTG TTT GTA TTC TCT AGC ATT 48
Met Glu Asn Leu Lys Asp Phe Tyr Val Leu Phe Val Phe Ser Ser Ile
-20 -15 -10

```

CCC CTT ACA TTT CTA TTT CAG AAA TTG CCT TTT GTT TGG ATT KGA GAA 96  
 Pro Leu Thr Phe Leu Phe Gln Lys Leu Pro Phe Val Trp Ile Xaa Glu  
 -5 1 5 10

GAG ACT TTG GAG ACA TGG TAT TTG AAG AGC TGG 129  
 Glu Thr Leu Glu Thr Trp Tyr Leu Lys Ser Trp  
 15 20

## (2) INFORMATION FOR SEQ ID NO: 124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 293..346
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq LSIFSLVLPVCRM/HR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

ACAAITCCAG CTTATGTGTC CCTTTTATAA ACTTGTGATA CATTTTAACT GTGTATACAC 60  
 ATCTCTTGCC TCTATTGGTA GAGAGTATCT GSCAKGCCCTA GCATGTGCTG GATGTCATAT 120  
 CAGATACTCA GTGTTATTTA TTGGGCTTAC AGTGATAACC AAAGCTCACA TGTTTATGCA 180  
 CTCCCACTTC CATAAAGTGG AAGATGTCCC CTCTGCCTCT TCTCTCATCC CTCCTCAAAG 240  
 CAGCAGGAGT GACTTACCTG ATTGACCACT TTAAGACTAT ATCTGAGCAG GC ATG CCA 298  
 Met Pro

CAG TAC TGT CTC AGC ATC TTC TCT CTT GTG CTG CCT GTC TGC AGG ATG 346  
 Gln Tyr Cys Leu Ser Ile Phe Ser Leu Val Leu Pro Val Cys Arg Met  
 -15 -10 -5

CAG AGG 352  
 His Arg

## (2) INFORMATION FOR SEQ ID NO: 125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 15..143

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.8  
seq LLAFGTSCSVVLY/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

```

GACCAGTTGG CGAC ATG GTG GCA CCC GTG CTG GAG ACT TCT CAC GTG TTT 50
 Met Val Ala Pro Val Leu Glu Thr Ser His Val Phe
 -40 -35

TGC TGC CCA AAC CGG GTG CGG GGA GTC CTG AAC TGG AGC TCT GGG CCC 98
Cys Cys Pro Asn Arg Val Arg Gly Val Leu Asn Trp Ser Ser Gly Pro
-30 -25 -20

AGA GGA CTT CTG GCC TTT GGC ACG TCC TGC TCC GTG GTG CTC TAT GAC 146
Arg Gly Leu Leu Ala Phe Gly Thr Ser Cys Ser Val Val Leu Tyr Asp
-15 -10 -5 1

CCC CTG GGT TGT TGT TAC CAA CTT GAA TGG TCA CAC CGC CCG TTC CGG 194
Pro Leu Gly Cys Cys Tyr Gln Leu Glu Trp Ser His Arg Pro Phe Arg
 5 10 15

```

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 134..247

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.8  
seq LSWLITWFGHXLS/DF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

```

ATTGTGGTCA CATTCTGCT GGTGGTAGGC GAGAGGCTGG CAACATCCCT GGTAGAAAAA 60

```

```

TTATCTACCC ACCACCTCAG GCATTTTATG GATCCAVCAA TGGRACAACA CCAMSCATAT 120
ATTAAACTAT CTG ATG CCC ATC ATT GAC CAG GTG AAT CCA GAG CTC CAT 169
 Met Pro Ile Ile Asp Gln Val Asn Pro Glu Leu His
 -35 -30

GAC TTC ATG CAG AGT GCT GAG GTA GGG ACC ATC TTT GCC CTC AGC TGG 217
Asp Phe Met Gln Ser Ala Glu Val Gly Thr Ile Phe Ala Leu Ser Trp
-25 -20 -15

CTC ATC ACC TGG TTT GGG CAT GWM CTG TCT GAC TTC AGG CAC GTC GTG 265
Leu Ile Thr Trp Phe Gly His Xaa Leu Ser Asp Phe Arg His Val Val
-10 -5 1 5

CGG TTA TAT GAC TTC TTC CTR GCC TGC CAC CCA CTG ATG CCG ATT TAC 313
Arg Leu Tyr Asp Phe Phe Leu Ala Cys His Pro Leu Met Pro Ile Tyr
10 15 20

TTT GCA GCC GTG ATT GTG TTG TAT CGC GAG CAG 346
Phe Ala Ala Val Ile Val Leu Tyr Arg Glu Gln
25 30

```

## (2) INFORMATION FOR SEQ ID NO: 127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 63..209
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq GLCVLVPCXSXX/WR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```

AAATKKKKKG AGCATTTTCT TCCCTGACAG CCGGACCTGG KACTGGGCTG GGGCCCTGGC 60
GG ATG GAG ACA TKC TGC CCC TGC TGC TGC TGC CCC TGC KGT GGG GDN 107
 Met Glu Thr Xaa Cys Pro Cys Cys Cys Cys Pro Cys Xaa Gly Xaa
 -45 -40 -35

GGG TCC CTG CAG GAG AAG CCA GTK TAC GAG CTG CAA GTG CAG AAG TCG 155
Gly Ser Leu Xaa Xaa Lys Pro Val Tyr Glu Leu Gln Val Gln Lys Ser
-30 -25 -20

GTG ACG GTG CAG GAG GGC CTG TGC GTC CTT GTG CCC TGC TCC TKC TCT 203
Val Thr Val Gln Glu Gly Leu Cys Val Leu Val Pro Cys Ser Xaa Ser

```

|                                                                 |     |    |     |
|-----------------------------------------------------------------|-----|----|-----|
| -15                                                             | -10 | -5 |     |
| TAS SCC TGG AGA TCC TGG TAT TCC TCT CCC CCA CTC TAC GTC TAC TGG |     |    | 251 |
| Xaa Xaa Trp Arg Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp |     |    |     |
| 1                                                               | 5   | 10 |     |
| TTC CGG GAC GGG GAG ATC CCA TAC TAC GCT GAG GTT GTG GCC ACA AAC |     |    | 299 |
| Phe Arg Asp Gly Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn |     |    |     |
| 15                                                              | 20  | 25 | 30  |
| AAC CCA GAC AGA AGA KTG AAG SMD KAK AYY CAK KGG CCG ATT CCG CCT |     |    | 347 |
| Asn Pro Asp Arg Arg Xaa Lys Xaa Xaa Xaa Xaa Xaa Pro Ile Pro Pro |     |    |     |
| 35                                                              | 40  | 45 |     |
| CCT TGG GGA TGT CCA GAA GAA GAA CTG                             |     |    | 374 |
| Pro Trp Gly Cys Pro Glu Glu Glu Leu                             |     |    |     |
| 50                                                              | 55  |    |     |

## (2) INFORMATION FOR SEQ ID NO: 128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 295..345
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq IYFFACFXSLTSS/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

|                                                                    |     |    |
|--------------------------------------------------------------------|-----|----|
| ATTTTCAGTG CAGCCTGCCA GACCTCTTCT GGAGGAAGAC TGGACAAAGG GGGTCACACA  | 60  |    |
| TTCCTTCCAT ACGSTTGAGC CTCTACCTGC CTGGTGCTGG TCACAGTTCA GCTTCTTCAT  | 120 |    |
| GRWKGGTGGA TCCCAATGGC AATGAATCCA GTGCTACATA CTTCACTCTA ATAGGCCTCC  | 180 |    |
| CTGSTTTAGA AGAGGCTCAG TTCTGGTTGG CCTTCCCATTT GTGCTCCCTC TACCTTATTG | 240 |    |
| CTGTGCTAGG TAACTTGACA ATCATCTACA TTGTGCGGAC TGAGCACAGC CTGC ATG    | 297 |    |
|                                                                    | Mat |    |
| AGC CCA TGT ATA TAT TTC TTT GCA TGC TTT CAN NNA TTG ACA TCC TCA    | 345 |    |
| Ser Pro Cys Ile Tyr Phe Phe Ala Cys Phe Xaa Xaa Leu Thr Ser Ser    |     |    |
| -15                                                                | -10 | -5 |
| TCT CCA CCT CAT CCA TGC CCA AAA TGC TGG CCA TCT TCT GGT TCA ATT    | 393 |    |
| Ser Pro Pro His Pro Cys Pro Lys Cys Trp Pro Ser Ser Gly Ser Ile    |     |    |

1

5

10

15

CCA CTA  
Pro Leu

399

## (2) INFORMATION FOR SEQ ID NO: 129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 12..92
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq VLKCLSFSXPSP/LP/GF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

AAGCAACCGG G ATG GGA CGG GGA GAG AGG AGG CAC TAC TGG GGA CCT AAG 50  
Met Gly Arg Gly Glu Arg Arg His Tyr Trp Gly Pro Lys  
-25 -20 -15

CTG GTT CTC AAA TGC CTC TCC TTT TCS SCT CCA AGC CTC CCA GGC TTC 98  
Leu Val Leu Lys Cys Leu Ser Phe Ser Xaa Pro Ser Leu Pro Gly Phe  
-10 -5 1

CTA TGG TCC CTA 110  
Leu Trp Ser Leu  
- 5

## (2) INFORMATION FOR SEQ ID NO: 130:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(B) LOCATION: 9..164  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.7  
 seq LLAKALHLLKSSC/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

```

AGCCTGCG ATG TCT CAA GAT GGC GGA STG GGC GAA TTA AAG CAC ATG GTG 50
Met Ser Gln Asp Gly Gly Xaa Gly Glu Leu Lys His Met Val
 -50 -45 -40

ATG AGT TTC CGG GTG TCT GAG CTC CAG GTG CTT CTT GGC TTT GCT GGC 98
Met Ser Phe Arg Val Ser Glu Leu Gln Val Leu Leu Gly Phe Ala Gly
 -35 -30 -25

CGG AAC AAG AGT GGA CGG AAG CAC GAG CTC CTG GCC AAG GCT CTG CAC 146
Arg Asn Lys Ser Gly Arg Lys His Glu Leu Leu Ala Lys Ala Leu His
 -20 -15 -10

CTC CTG AAG TCC AGC TGT GCC CCT AGT GTC CAG ATG AAG ATC AAA GAG 194
Leu Leu Lys Ser Ser Cys Ala Pro Ser Val Gln Met Lys Ile Lys Glu
 -5 1 5 10

CTT TAC CGA CGA CGC TTT CCC CGG AAG ACC CTG GGG CCC TCT GAT CTC 242
Leu Tyr Arg Arg Arg Phe Pro Arg Lys Thr Leu Gly Pro Ser Asp Leu
 15 20 25

TCC CTA AAG 251
Ser Leu Lys

```

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 272 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 18..224  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.6  
 seq LGPSLSSLPSALS/LM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```

TATTTGGCCC CAAGCCG ATG CAT CAC AGG ATG AAT GAA ATG AAC CTG AGT 50
Met His His Arg Met Asn Glu Met Asn Leu Ser
 -65 -60

```



```

CCA GTG GGG ATG GAG CAG CTG ACT TCA TCC TCT GTG AGC AAT GCC TTG 98
Pro Val Gly Met Glu Gln Leu Thr Ser Ser Ser Val Ser Asn Ala Leu
 -55 -50 -45

CCA GTC TCA GGA AGT CAC CTG GGA TTG GCT GCC TCA CCC ACT CAC AGT 146
Pro Val Ser Gly Ser His Leu Gly Leu Ala Ala Ser Pro Thr His Ser
 -40 -35 -30

GCC ATC CCT GCC CCA GGC CTC CCA GTG GCA ATT CCA AAC CTG GGT CCC 194
Ala Ile Pro Ala Pro Gly Leu Pro Val Ala Ile Pro Asn Leu Gly Pro
 -25 -20 -15

TCC CTG AGC TCT CTG CCT TCT GCT CTG TCT TTA ATG CTA CCA ATG GGT 242
Ser Leu Ser Ser Leu Pro Ser Ala Leu Ser Leu Met Leu Pro Met Gly
 -10 -5 1 5

DTT GGG GAT CGA GGG GTG ATG TGT GGG TTA 272
Xaa Gly Asp Arg Gly Val Met Cys Gly Leu
 10 15

```

## (2) INFORMATION FOR SEQ ID NO: 132:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 62..118
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq IWNLFSLFSTSTT/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```

ACATCCTTGA TTCTTTACTT TCTCTTAACA CCTGTATCC AGCTGGTCAT AAATCTAGCA 60
G ATG CTA CAT TCA GAT AAC ATC TGG AAT CTA TTT TCC CTA TTT TCT ACT 109
Met Leu His Ser Asp Asn Ile Trp Asn Leu Phe Ser Leu Phe Ser Thr
 -15 -10 -5

TCT ACT ACC CTG CCC CGG 127
Ser Thr Thr Leu Pro Arg
 1

```

## (2) INFORMATION FOR SEQ ID NO: 133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 4..75
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq FHSAAGWSGGGQA/CG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATT ATG CAA CCC GCC TCC CCG CCC GCC CGG TGG AGC TTC CAC TCG GCT | 48  |
| Met Gln Pro Ala Ser Pro Pro Ala Arg Trp Ser Phe His Ser Ala     |     |
| -20 -15 -10                                                     |     |
| GGC GGC TGG AGC GGC GGC GGG CAG GCG TGC GGA GGA CAC TCC TGC GAC | 96  |
| Ala Gly Trp Ser Gly Gly Gly Gln Ala Cys Gly Gly His Ser Cys Asp |     |
| -5 1 5                                                          |     |
| CAG GTA CTG GCT GTG ATC GAA CTT CTC AAC CCT CTC AGG             | 135 |
| Gln Val Leu Ala Val Ile Glu Leu Asn Pro Leu Arg                 |     |
| 10 15 20                                                        |     |

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 138..191
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq LLAGSISHMFSQA/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

|                                                                   |    |
|-------------------------------------------------------------------|----|
| ATATTTTGCC TTAGCAGCCT GGGCTTCGGA ACTGGGCTTG CCCTGTAGCA GSTCACTTGC | 60 |
|-------------------------------------------------------------------|----|

ACCTTTCTGC CACAGATGAC GGAAACATTT AAAGTTATGG ATTGTGTCTC TGCATCCTCT 120

TCCCTTCACA CCAGCCA ATG TGT TTT TCA TTT CTC TTG GCT GGC TCA ATT 170  
 Met Cys Phe Ser Phe Leu Leu Ala Gly Ser Ile  
 -15 -10

TCC CAC ATG TTC TCC CAA GCT CTT CTT CTC CAC TCC CCA GGG CTT CCC 218  
 Ser His Met Phe Ser Gln Ala Leu Pro Leu His Ser Pro Gly Leu Pro  
 -5 1 5

ACC ACA AAC CGC ACG 233  
 Thr Thr Asn Arg Thr  
 10

## (2) INFORMATION FOR SEQ ID NO: 135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 137..199
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
 seq SILFHCSVCLFLC/QY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

ATATGGCAAG AGATAGAGAT CTAGTTTCAT TCTTCTGCAT ATGGATATCC AATTTTCCCA 60

GCACCATTTA TTGAAGAGAC AGTCCTTTTG CCAGTKTATG TTCTTGGCAA CTTTGTTGAA 120

AATGCATTIA CTGTAG ATG TAT GGA TTC ATT ATT GGG TTA TCT ATT CTG TTC 172  
 Met Tyr Gly Phe Ile Ile Gly Leu Ser Ile Leu Phe  
 -20 -15 -10

CAT TGT TCT GTG TGT CTG TTT TTA TGC CAG TAC CAT GCC TGG 214  
 His Cys Ser Val Cys Leu Phe Leu Cys Gln Tyr His Ala Trp  
 -5 1 5

## (2) INFORMATION FOR SEQ ID NO: 136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 139..210  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.5  
seq SLLGCXLAININT/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```

ATCCTATTGT GTCGTGTAGC TTGTTCTCTA TTTTATAGGT CATTTAAAAT AAAACTCACC 60
TTTGACTTTG ITTAGTCTCT GTTACATGTT TGCITTTTGT TCGTTTATG TTTGTACATT 120
TCTCATGTKT TTCTKKCT ATG TCT TTT GGT KGT ATT CTA ACT TTT AGA GTC 171
 Met Ser Phe Gly Xaa Ile Leu Thr Phe Arg Val
 -20 -15

TCT TTA TTG GGA TGT CNT CTA GCG ATA AAT ATA AAT ACA TTT CCC TCT 219
Ser Leu Leu Gly Cys Xaa Leu Ala Ile Asn Ile Asn Thr Phe Pro Ser
 -10 -5 1

AAC AAC CAC TTG 231
Asn Asn His Leu
 5

```

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 12..77  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq LGRLCAGSSGVXG/AR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```

AAAAGCGAGC C ATG GGT GTC TAC GTC GGG ATG CTG CGC CTG GGG AGG CTG 50
 Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu

```

|                                                                 | -20 | -15 | -10 |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| TGC GCC GGG AGC TCG GGG GTC STG GGG GGC CGG GCC GSC CTC TCT CGG |     |     |     | 98  |
| Cys Ala Gly Ser Ser Gly Val Xaa Gly Ala Arg Ala Xaa Leu Ser Arg |     |     |     |     |
|                                                                 | -5  | 1   | 5   |     |
| AGT TGG CAG GAA GCC AGG TTG CAG GGT GTC CGC TTC CTC AGT TCC AGA |     |     |     | 146 |
| Ser Trp Gln Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Ser Ser Arg |     |     |     |     |
|                                                                 | 10  | 15  | 20  |     |
| GAG GTG GAT CGC ATG GTC TCC ACG CCC ATC GGA GGC CTC ACC TAC GTT |     |     |     | 194 |
| Glu Val Asp Arg Met Val Ser Thr Pro Ile Gly Gly Leu Ser Tyr Val |     |     |     |     |
|                                                                 | 25  | 30  | 35  |     |
| CAG GGG TGC ACC AAA AAG CAT CTT AAC AGC AAG ACT GTG GGC CAG TGC |     |     |     | 242 |
| Gln Gly Cys Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly Gln Cys |     |     |     |     |
|                                                                 | 40  | 45  | 50  | 55  |
| CTG GAG ACC ACA GCA CAG AGG GTC CCG                             |     |     |     | 269 |
| Leu Glu Thr Thr Ala Gln Arg Val Pro                             |     |     |     |     |
|                                                                 | 60  |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 187..255
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq LVSIFFFWEVTNA/FL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

|                                                                   |             |
|-------------------------------------------------------------------|-------------|
| AGATAATTTT GATGAAACCA AGAGGCACGT CTTTCTACAT ACTTCTCTTC ATCKYCMWTT | 60          |
| CCTASTGTTT TNGTTTATKT TTTTAAATA ATGCCCATGT CTCCTGCTGT CATTTCTCTGA | 120         |
| GACCACCAAA TAGTTTAATA CCTGGAGTCA GAGATAAGAA TAAACAGGCT TAAGATACTT | 180         |
| TAAATA ATG TTC AAT ACT ATA TAC TTG GTC ATA TCA TTA GTG AGC ATA    | 228         |
| Met Phe Asn Thr Ile Tyr Leu Val Ile Ser Leu Val Ser Ile           |             |
|                                                                   | -20 -15 -10 |
| TTT TTC TTT TGG GAA GTA ACT AAT GCT TTC CTT AAG GCC AGG CGT TGG   | 276         |
| Phe Phe Phe Trp Gln Val Thr Asn Ala Phe Leu Lys Ala Arg Arg Trp   |             |
|                                                                   | -5 1 5      |

## (2) INFORMATION FOR SEQ ID NO: 139:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 36..101
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq SLPLTTGSSWSLS/SQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```

ACCITCTCAA GAACTGTGTT CACCCACTTC CCCAC ATG GCC CTT CCA CCC AAG 53
 Met Ala Leu Pro Pro Lys
 -20

GGA TGT GGT AGT CTC CCT TTG ACT ACT GGG TCT TCC TGG AGC CTT TCT 101
Gly Cys Gly Ser Leu Pro Leu Thr Thr Gly Ser Ser Trp Ser Leu Ser
-15 -10 -5

TCT CAA ATA GGA AGC CCT GCT ATT TCC AAC CCT AGG 137
Ser Gln Ile Gly Ser Pro Ala Ile Ser Asn Pro Arg
 1 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 44..91
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq FLSWASEFLAPLLR/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```

GTCATTGTGC CGTTTCTTCC CCCTTGCCAA TTTTAAATT ASA ATG TTT GTC TTT 55
 Met Phe Val Phe
 -15

TTG TCT TGG GCA AGT TTC TTA GCC CCT CTA CTG AGG AGC CCA TTT CTT 103
Leu Ser Trp Ala Ser Phe Leu Ala Pro Leu Leu Arg Ser Pro Phe Leu
-10 -5 1

CAT TGT CTA ATG GGG ATG CCA GGG 127
His Cys Leu Met Gly Met Pro Gly
5 10

```

## (2) INFORMATION FOR SEQ ID NO: 141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 150..233
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq LLSCSPLXPLGKS/GF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

```

AAKAGTCAGC AGGAGTKAGT TCAGGAATCC TCGGGACAAG GCACTTTCCT GAGCACTGGA 60

CCAGCGACCT CTTGGCTTCC AGGGAGGACA CACAGCCATC ATGGWACCCA THTCTCAGAA 120

GAGTCCAGGC AAACAGTTTA CATTTTCTT ATG AWA ATG AAG TCT GCA AAC AAG 173
 Met Xaa Met Lys Ser Ala Asn Lys
 -25

ATT ACT TTA TTA ART CAC CAC CTT CTC AGC TGT TCT CCT CTG TGW CCT 221
Ile Thr Leu Leu Xaa His His Leu Leu Ser Cys Ser Pro Leu Xaa Pro
-20 -15 -10 -5

CTT GGA AAA AGC GGT TTT TCA TCC TGT CAA AGG CTG GCG AAA AGA GCT 269
Leu Gly Lys Ser Gly Phe Ser Ser Cys Gln Arg Leu Gly Lys Arg Ala
1 5 10

TTA GTC TTT CCT ATT ATR AAG NCC ATC ATC ACC 302
Leu Val Phe Pro Ile Xaa Lys Xaa Ile Ile Thr
15 20

```

## (2) INFORMATION FOR SEQ ID NO: 142:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 150..245
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq SFLLLFIVIPQTP/RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

```

AATTGATAA CATCAGCTAA TATTTTCAA AGTTAGATTT TTGAGGTATA ATTTACATAA 60
GAGTTACTCT TTCTAGAGGT ATAGTTGAAT GCATTTTCAC AAATGTGTAC AATTGATAA 120
CCACCAMCAT WAWTCTAGAW ATATAGGTA ATG TGT AAT TAT AAT ATA TAT GTA 173
 Met Cys Asn Tyr Asn Ile Tyr Val
 -30 -25
CTA TAT AAT ATA GGA TAT TTA TAC CAC CCA AAA AGT TTT CTC TTG CTT 221
Leu Tyr Asn Ile Gly Tyr Leu Tyr His Pro Lys Ser Phe Leu Leu Leu
 -20 -15 -10
TTT ATA GTC ATT CCC CAA ACC CCA CGT CCG 251
Phe Ile Val Ile Pro Gln Thr Pro Arg Pro
 -5 1

```

## (2) INFORMATION FOR SEQ ID NO: 143:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide



(B) LOCATION: 84..164  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.2  
 seq PLLAAPLLRSLLP/RX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

```

AACTGAACAG CGGASC GGAC GGGGATCGCC GCGGGCGGCG AAGCGGAGGC GGCCACAGGC 60
CCGGCGGTCT CCGAGATGTC ACG ATG GCT GTG GCC ATG GTC AAA CTG TGT GAA 113
 Met Ala Val Ala Met Val Lys Leu Cys Glu
 -25 -20

AGA GCG GGT CTG CCG CTA CTT GCT GCA CCA CTA CTT AGG TCA CTT CTT 161
Arg Ala Gly Leu Pro Leu Leu Ala Ala Pro Leu Leu Arg Ser Leu Leu
 -15 -10 -5

CCA AGA GMA CCT CAG CCT GGA CCA GCT CAG CCT CGA TCT GTA CAA GGG 209
Pro Arg Xaa Pro Gln Pro Gly Pro Ala Gln Pro Arg Ser Val Gln Gly
 1 5 10 15

CAG CGT TGC CCT GCG AGA CAT CCA CCT GGA AAT CTG GTC TGT GAA CGA 257
Gln Arg Cys Pro Ala Arg His Pro Pro Gly Asn Leu Val Cys Glu Arg
 20 25 30

GGT GCT RGA GTC AAT GGA GTC ACC GCT GGA GCT RGT GGA ARG CTT CGT 305
Gly Ala Xaa Val Asn Gly Val Thr Ala Gly Ala Xaa Gly Xaa Leu Arg
 35 40 45

GGG CTC CAT CGA GGT DGC CGT GCC CTG GGC TGC TCT GCT CAC CGA CCA 353
Gly Leu His Arg Gly Xaa Arg Ala Leu Gly Cys Ser Ala His Arg Pro
 50 55 60

MTG CAC AGT GCG CGT GTC CGG CCT CCA GCT 383
Xaa His Ser Ala Arg Val Arg Pro Pro Ala
 65 70

```

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 99..464
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
 seq DVLLGLLKDVLLA/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```

TAAACTTCTG AAAGAAAGAG AAGATCTTCC TATATGGAAA GAAAAATACT CCTTTATGGA 60
GAACTGTGCTT CAAAATCAAA TCGTGATTGT TTCAGGAG ATG CTA AAT GTG GTA AGA 116
 Met Leu Asn Val Val Arg
 -120

GCG CTC AGG KTY CCT CAG TGG TGT GCT GAA TAT TGT CTT TCC ATC CAC 164
Ala Leu Arg Xaa Pro Gln Trp Cys Ala Glu Tyr Cys Leu Ser Ile His
-115 -110 -105

TAC CAG CAC GGG GGC GTG ATA TGC ACA CAG GTC CAC AAG CAG ACT GTG 212
Tyr Gln His Gly Gly Val Ile Cys Thr Gln Val His Lys Gln Thr Val
-100 -95 -90 -85

GTC CAG CTC GCC CTG CGG GTG GCG GAT GAA ATG GAT GTT AAC ATT GGT 260
Val Gln Leu Ala Leu Arg Val Ala Asp Glu Met Asp Val Asn Ile Gly
 -80 -75 -70

CAT GAG GTT GGC TAC GTG ATC CCT TTC GAG AAC TGC TGT ACC AAC GAA 308
His Glu Val Gly Tyr Val Ile Pro Phe Glu Asn Cys Cys Thr Asn Glu
 -65 -60 -55

ACA ATC CTG AGG TAT TGT ACT GAT GAT ATG CTG CAA AGA GAA ATG ATG 356
Thr Ile Leu Arg Tyr Cys Thr Asp Asp Met Leu Gln Arg Glu Met Met
 -50 -45 -40

TCC AAT CCT TTT TTG GGT AGC TAT GGG GTC ATC ATC TTA GAT GAT ATT 404
Ser Asn Pro Phe Leu Gly Ser Tyr Gly Val Ile Ile Leu Asp Asp Ile
-35 -30 -25

CAT GAA AGA AGC ATT GCA ACT GAT GTG TTA CTT GGA CTT CTT AAA GAT 452
His Glu Arg Ser Ile Ala Thr Asp Val Leu Leu Gly Leu Leu Lys Asp
-20 -15 -10 -5

GTT TTA CTA GCA AGA CCA GAA CTG AAG 479
Val Leu Leu Ala Arg Pro Glu Leu Lys
 1 5

```

(2) INFORMATION FOR SEQ ID NO: 145:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 107..187
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.2  
seq AGLCIGSTSYVHG/DI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```

ATTGGGAGCA GCAGCATCTA CTTCACAGAC CAGTGTCCAG TTAATTGTST TTGTGGCAAT 60
CATCCTACAT AAGGCACCAG CTGCTTTTGG ACTGGTTTCC TTCTTG ATG CAT GCT 115
 Met His Ala
 -25

GGC TTA GAG CGG RAW TCG AWT CAG AAA GCA CTT GCT GST CTT TGC ATT 163
Gly Leu Glu Arg Xaa Ser Xaa Gln Lys Ala Leu Ala Gly Leu Cys Ile
 -20 -15 -10

GGC AGC ACC AGT TAT GTC CAT GGT GAC ATA CTT AGG ACT GAG CGG 208
Gly Ser Thr Ser Tyr Val His Gly Asp Ile Leu Arg Thr Glu Arg
 -5 1 5

```

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 285 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Prostate

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 151..255  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.2  
 seq LLGSLSLWRWSAM/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```

AATTGCTGGG CTCGAAGCAC AGGAGAGACC AGTCCTTCCT TGTCTCCACT GGGCTGKTAA 60
GTGCTTCTTT CCAAGGACK TCCATCCCTT CCCCAGGCTT TATGGTTCCA GTCCTTCTAC 120
CATTCTGGAA GCTCCCTAGA ATCTCCTGGA ATG CTT AAT GGA CCT TTC CAG CAC 174
 Met Leu Asn Gly Pro Phe Gln His
 -35 -30

CGA AAT TCA AGA ATT ATG ACT CAT CGG TCA GCA GAA AAG ACC CTG CTG 222
Arg Asn Ser Arg Ile Met Thr His Arg Ser Ala Glu Lys Thr Leu Leu
 -25 -20 -15

GGA TCT TTG AGC TTG TGG AGG TGG TCG GCA ATG GAA CCT ACG GAC AGG 270
Gly Ser Leu Ser Leu Trp Arg Trp Ser Ala Met Glu Pro Thr Asp Arg
 -10 -5 1 5

```

TGT ACA AGG GTA GGG  
Cys Thr Arg Val Gly  
10

285

## (2) INFORMATION FOR SEQ ID NO: 147:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 44..175
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq IAVGLTCQHVSHA/IS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAGGTTGTAG ACGCTGCGGC CCGGCCCGGC GGGTAAATAA CAG ATG CGC GTG AAA | 55  |
| Met Arg Val Lys                                                 |     |
| GAT CCA ACT AAA GCT TTA CCT GAG AAA GCC AAA AGA AGT AAA AGG CCT | 103 |
| Asp Pro Thr Lys Ala Leu Pro Glu Lys Ala Lys Arg Ser Lys Arg Pro |     |
| -40 -35 -30 -25                                                 |     |
| ACT GTA CCT CAT GAT GAA GAC TCT TCA GAT GAT ATT GCT GTA GGT TTA | 151 |
| Thr Val Pro His Asp Glu Asp Ser Ser Asp Asp Ile Ala Val Gly Leu |     |
| -20 -15 -10                                                     |     |
| ACT TGC CAA CAT GTA AGT CAT GCT ATC AGC GTG AAT CAT GTA AAG AGA | 199 |
| Thr Cys Gln His Val Ser His Ala Ile Ser Val Asn His Val Lys Arg |     |
| -5 1 5                                                          |     |
| GCA ATA GCT GAG AAT CTG TGG TCA GTT TGC TCA GAA TGT TTA AAA GAA | 247 |
| Ala Ile Ala Glu Asn Leu Trp Ser Val Cys Ser Glu Cys Leu Lys Glu |     |
| 10 15 20                                                        |     |
| AGA AGA TTC TAT GAT GGG CAG CTA GTA CTT ACT TCT GAT ATT TGG TTG | 295 |
| Arg Arg Phe Tyr Asp Gly Gln Leu Val Leu Thr Ser Asp Ile Trp Leu |     |
| 25 30 35 40                                                     |     |
| TGC CTC AAG TGT GGC TTC CAG GGA TGT GGT AAA AAC TCA GAA AGC CAA | 343 |
| Cys Leu Lys Cys Gly Phe Gln Gly Cys Gly Lys Asn Ser Glu Ser Gln |     |
| 45 50 55                                                        |     |
| CAT TCA TTG AAG CAC TTT AAG AGT TCC AGA ACA GAG CCC CAT TGT ATT | 391 |
| His Ser Leu Lys His Phe Lys Ser Ser Arg Thr Glu Pro His Cys Ile |     |
| 60 65 70                                                        |     |

ATA ATT AAT CTG AGC ACA  
 Ile Ile Asn Leu Ser Thr  
 75

409

## (2) INFORMATION FOR SEQ ID NO: 148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 184..267
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq FSLALSMKGTG/KV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

ACATAATCGG CCTTTATGTT ACACTGCCTG GCCAGCCCCCT GTTATTCTAG TGCATAATTG 60  
 ATGGTGCTCA CAAGTGGAAA AGTTAGAAAA GCGGAAGTAA TGTGACGCAG CAGTGCCATG 120  
 RAGCSCCGG DVCCCCGGCA GIGAGGGCAA TGCAGAGATG GGCTGCTGCT GGCTACCGCC 180  
 AGG ATG CCT CAG AAG GGC CTG GGC TTA CTT GGC ATC TTG TCA GGA GAC 228  
 Met Pro Gln Lys Gly Leu Gly Leu Gly Ile Leu Ser Gly Asp  
 -25 -20 -15  
 TTT TCC CTT CTT GCT TTG TCC ATG CTG AAA GGG ACA GGA AAG GTA GGC 276  
 Phe Ser Leu Leu Ala Leu Ser Met Leu Lys Gly Thr Gly Lys Val Gly  
 -10 -5 1  
 GGG 279  
 Gly

## (2) INFORMATION FOR SEQ ID NO: 149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 69..233  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq AALCGISLSQLFP/EP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```

AAGAACCTGA GCAGCCTGTC TTCAGACAGA GAGAGGCCCA CGGCTGTTTC TTGAAAYTGG 60
CGCTGSGA ATG GCC ATG TGG AAC AGG CCA TGB BAG ANG CTG CCT CAG CAG 110
Met Ala Met Trp Asn Arg Pro Xaa Xaa Xaa Leu Pro Gln Gln
-55 -50 -45
CCT CTS STA GCT GAG CCC ACT GCA GAG GGG GAG CCA CAC CTG CCC ACG 158
Pro Leu Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr
-40 -35 -30
GGC CSG GAS BYG ACT GAG GCC AAC CGC TTC GCC TAT GCT GGC CTC TGT 206
Gly Arg Xaa Xaa Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys
-25 -20 -15 -10
GGC ATC TCC CTG TCC CAG TTA TTT CCT GAA CCC GAA CAC AGC TCC TTC 254
Gly Ile Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe
-5 1 5
TGC ACA GAG TTC ATG GCA GGC CTG GTG SKM TGG CTG GAG TTG TCT GAA 302
Cys Thr Glu Phe Met Ala Gly Leu Val Xaa Trp Leu Glu Leu Ser Glu
10 15 20
GCT GTC TTG CCA ACC ATG ACT GCT 326
Ala Val Leu Pro Thr Met Thr Ala
25 30

```

## (2) INFORMATION FOR SEQ ID NO: 150:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 126..182  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq LLLSPWVTVPVWS/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```

CCTACTGCTT AAGGGGATTT AGCATCATCC AAGCAGGGTA AACTTTTGTT TTGTTAAAAG 60
AAAAATGTGT TATTCAGTT GGTGTCCCCA GTGTAGCTA ACACATCTGG AATGCACATA 120
CCAAA ATG CTG TGC TTT GSA GAC CTG CTT TTG TCA CCG TGG GTA ACC GTT 170
 Met Leu Cys Phe Gly Asp Leu Leu Leu Ser Pro Trp Val Thr Val
 -15 -10 -5

CCC GTC TGG TCC AGT AGC CCG TGG 194
Pro Val Trp Ser Ser Ser Pro Trp
 1

```

## (2) INFORMATION FOR SEQ ID NO: 151:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 27..107
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq LIYFLGLAAQTYF/RS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```

AAGTTAGGTT TAAAGTTTCC TCATTA ATG CAG GAA AAT GCT CAT AAC CTG AGG 53
 Met Gln Glu Asn Ala His Asn Leu Arg
 -25 -20

CTT TTC AAG TGT TTA TTA ATT TAC TTT CTG GGG CTG GCT GCT GAT ACT 101
Leu Phe Lys Cys Leu Leu Ile Tyr Phe Leu Gly Leu Ala Ala Asp Thr
 -15 -10 -5

TAT TTC ASA TCA AAG AGA AAG CCT GTG TCT TTC GTA GTT ACT GTG KKG 149
Tyr Phe Arg Ser Lys Arg Lys Pro Val Ser Phe Val Val Thr Val Xaa
 1 5 10

CMA GGA AMC TAT GCC ACA GGG 170
Xaa Gly Xaa Tyr Ala Thr Gly
 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 127..303
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq SVATALFPPLCIS/TG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```

ACCAAGTCCT CCCAAGTTAT TAACTGGTCA AAAAGGMTTA AAGGMTTAGT TCTTAATAGT 60
TAAGATGCCA CCCATTCAGG GTTTTTTGCT TTCTAAGAGG GAACTTTTAC AGGCATAATT 120
GAGAGA ATG CAT ACA TGC TCT CTA CCT TGT CTT CTC TTT GCT CAG CTG 168
 Met His Thr Cys Ser Leu Pro Cys Leu Leu Phe Ala Gln Leu
 -55 -50

CTA GAA TTT TGT AGC TTT CCT CCA GAT GTG CCT CAT AAC TGT GCG CCT 216
Leu Glu Phe Cys Ser Phe Pro Pro Asp Val Pro His Asn Cys Ala Pro
-45 -40 -35 -30

ATT GTC TCA GTC AGG CCG CCT AAT ATT GTA GCA GCC TTT GAA GGG TGC 264
Ile Val Ser Val Arg Pro Pro Asn Ile Val Ala Ala Phe Glu Gly Cys
 -25 -20 -15

TCT GTA GCC ACT GCT CTT TTT CCT CCC TTG TGC ATC TCC ACA GGG AAT 312
Ser Val Ala Thr Ala Leu Phe Pro Pro Leu Cys Ile Ser Thr Gly Asn
 -10 -5 1

GAG 315
Glu

```

## (2) INFORMATION FOR SEQ ID NO: 153:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate



## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 35..138  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4  
 seq PLLGVLFFQGVYI/VF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```

AGTCGTTACC GGGASCTGTA AACAAAGGTGT GCAAGCATCT GAAGAGCTGC CGGG ATG 57
 Met

CAG CAG AGA GGA GCA SCT GGA ACC CGT GGC TGC GCT CTC TTC CCT CTG 105
Gln Gln Arg Gly Ala Ala Gly Ser Arg Gly Cys Ala Leu Phe Pro Leu
 -25 -20 -15

CTG GGC GTC CTG TTC TTC CAG GGT GTT TAT ATC GTC TTT TCC TTG GAG 153
Leu Gly Val Leu Phe Phe Gln Gly Val Tyr Ile Val Phe Ser Leu Glu
 -10 -5 1 5

ATT CGT GCA GAT GCC CAT GTC CGA GGT TAT GTT GGA GAA AAG ATC AAG 201
Ile Arg Ala Asp Ala His Val Arg Gly Tyr Val Gly Glu Lys Ile Lys
 10 15 20

TTG AAA TGC ACT TTC AAG TCA ACT TCA GAT GTC ACT GAC AAG CTT ACT 249
Leu Lys Cys Thr Phe Lys Ser Thr Ser Asp Val Thr Asp Lys Leu Thr
 25 30 35

ATA GAC TGG ACA TAT CGC CCT CCC AGC AGC AGC CAC ACA GTA TCA ATA 297
Ile Asp Trp Thr Tyr Arg Pro Pro Ser Ser Ser His Thr Val Ser Ile
 40 45 50

KTK CAT TAT CAG TCT TTC CAG TAC CCA ACC ACA GCA GGC ACA TTT 342
Xaa His Tyr Gln Ser Phe Gln Tyr Pro Thr Thr Ala Gly Thr Phe
 55 60 65

```

## (xii) INFORMATION FOR SEQ ID NO: 154:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 109..225  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
 seq LILNRS LPTASSS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```

AAAAATGTAC TGAATGTCCA CTTTGGGCCA GGCTGGGCAC CGAGGACACA GGGGAACATA 60
GACACAGTCC TGSTCACTGG GAAACTCACA GCCTGTTGGG AAAGAAAG ATG CAM GAV 117
 Met Xaa Xaa

AGT ATC TTC ATT TCA GAA AAA TAT GGA CTC TGC CCG TCT AAG ACT CCC 165
Ser Ile Phe Ile Ser Glu Lys Tyr Gly Leu Cys Pro Ser Lys Thr Pro
-35 -30 -25

ATA ATG AAA ATG CTC CCG TCT TTG ATC CTG AAC CGG TCA TTG CCC ACT 213
Ile Met Lys Met Leu Pro Ser Leu Ile Leu Asn Arg Ser Leu Pro Thr
-20 -15 -10 -5

GCT TCA AGC AGT TCC AGC AGG AAG GAC TTC CGC CTG CCT CAG ACC CGC 261
Ala Ser Ser Ser Ser Arg Lys Asp Phe Arg Leu Pro Gln Thr Arg
 1 5 10

CGG CGA ATC ATC ATG GTG CCT CGC AAG GAG GAT CAG ACA CCC CTT AAT 309
Arg Arg Ile Ile Met Val Pro Arg Lys Glu Asp Gln Thr Pro Leu Asn
15 20 25

CCT GCA TCC CAA CCT CAG GCT CCC CCA AAG CCC ATC CCC AGC TTS AAA 357
Pro Ala Ser Gln Pro Gln Ala Pro Pro Lys Pro Ile Pro Ser Xaa Lys
30 35 40

AGT YTG GAA GCT AGM GAT AYC AAS RGC AGC CAG AGG ACA BGA AGA CCT 405
Ser Leu Glu Ala Xaa Asp Xaa Xaa Xaa Ser Gln Arg Thr Xaa Arg Pro
45 50 55 60

GGG CTG AGC AGA GGT CGA AGC TGC 429
Gly Leu Ser Arg Gly Arg Ser Cys
65

```

(2) INFORMATION FOR SEQ ID NO: 155:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..350
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 99.1  
region 18..366  
id D83597  
vrt

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 127..186  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
 seq FFWVVLFSAGCKV/IT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```

ATTCTTTGTT CCAAGATCAC CCTTCTGAGT ACCTCTCTGG CTGCCAAATT GCCAGGGCCT 60
TCACASTTTG ATTTCATTTC TCAGCTCCAA GCATTAGGTA AACCCACCAA GCAATCCTAG 120
CCTGTG ATG GCG TTT GAC GTC ASC TGC TTC TTT TGG GTG GTG CTG TTT 180
Met Ala Phe Asp Val Ser Cys Phe Phe Trp Val Val Leu Phe
-20 -15 -10
TCT GCC GCG TGT AAA GTC ATC ACC TCC TGG GAT CAG ATG TAC ATT GAG 216
Ser Ala Gly Cys Lys Val Ile Thr Ser Trp Asp Gln Met Tyr Ile Glu
-5 1 5 10
AAA GAA GCC AAC AAA ACA TAT AAC TGT GAA AAT TTA GGT CTC AGT GAA 264
Lys Glu Ala Asn Lys Thr Tyr Asn Cys Glu Asn Leu Gly Leu Ser Glu
15 20 25
ATC CCT GAC ACT CTA CCA AAC ACA ACA GAA TTT TTG GAA TTC AGC TTT 312
Ile Pro Asp Thr Leu Pro Asn Thr Thr Glu Phe Leu Glu Phe Ser Phe
30 35 40
AAT TTT TTG CCT ACA ATT CAC AAT AGA ACC TCC AGC AGG 351
Asn Phe Leu Pro Thr Ile His Asn Arg Thr Ser Ser Arg
45 50 55

```

## (2) INFORMATION FOR SEQ ID NO: 156:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 410 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 96..1383  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
 seq IMNLTVMLDTAXG/KX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

```

AGAACCACGC CGCTTCCCAG TCTCTGTGCG AGGCGTGAAG CGCGGACCTT TCAACAAGGG 60

```

```

CTTTATTAAT TCTCAGGCTG CGGCGCTGGA AAGCG ATG GAG GTG GCG GCT AAT 113
 Met Glu Val Ala Ala Asn
 -95

TGC TCC CTA CGG CTC AAG AGA CCT CTG TTG GAT CCC CGC TTC GAG GGT 161
Cys Ser Leu Arg Val Lys Arg Pro Leu Leu Asp Pro Arg Phe Glu Gly
-90 -85 -80 -75

TAC AAG BTC TCT CTT GAG CCG CTG CCT TGT TAC CAG CTG GAG CTT GAC 209
Tyr Lys Xaa Ser Leu Glu Pro Leu Pro Cys Tyr Gln Leu Glu Leu Asp
 -70 -65 -60

GCA GCT GTG GCA KAG GTA AAA CTT CGA GAT GAT CAA TAT ACA CTG GAA 257
Ala Ala Val Ala Xaa Val Lys Leu Arg Asp Asp Gln Tyr Thr Leu Glu
 -55 -50 -45

CAC ATG CAT GCT TTT GGA ATG TAT AAT TAC CTG CAC TGT GAT TCA TGG 305
His Met His Ala Phe Gly Met Tyr Asn Tyr Leu His Cys Asp Ser Trp
 -40 -35 -30

TAT CAA GAC AGT GTC TAC TAT ATT GAT ACC CTT GGA AGA ATT ATG AAT 353
Tyr Gln Asp Ser Val Tyr Ile Asp Thr Leu Gly Arg Ile Met Asn
 -25 -20 -15

TTA ACA GTA ATG CTG GAC ACT GCC TTW GGR AAA MCA CGA GAG GTG TTT 401
Leu Thr Val Met Leu Asp Thr Ala Xaa Gly Lys Xaa Arg Glu Val Phe
-10 -5 1 5

CGA CTC CTA 410
Arg Leu Leu

```

## (2) INFORMATION FOR SEQ ID NO: 157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 63..179
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq VLAIGLLHIVLLS/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

```

AGGGGACCGA TCCCGGGCCG TTGATCTCG GCGCCACACG AACAGCAGAG AGGGGCATCA 60
GG ATG AAT GTC GGC ACA GCG CAC AGS DAG GTG AAC CCC AAC ACG CGG 107

```

```

Met Asn Val Gly Thr Ala His Xaa Xaa Val Asn Pro Asn Thr Arg
 -35 -30 -25

GTK ATG AAC ACC CGT GGC ATC TGG CTC TCC TAC GTG CTG GCC ATC GGT 155
Val Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly
 -20 -15 -10

CTC CTC CAC ATC GTG CTG CTG AGC ATC CCG TTT GTK AGT GTC CCT GTC 203
Leu Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val
 -5 1 5

GTC TGG ACC CTC ACC AAC CTC ATT CAC AAC ATG GGC ATG TAT ATC TTC 251
Val Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe
 10 15 20

CTG CAC ACG GTG AAG GGG WCA CCC TTT GAG ACC CCG GAC CAG GGC AAG 299
Leu His Thr Val Lys Gly Xaa Pro Phe Glu Thr Pro Asp Gln Gly Lys
 25 30 35 40

GGG AGG CTG CTW WCC CAC TGG TDA GCA GAT GGA TTA TGG GGT CCA GTT 347
Ala Arg Leu Leu Xaa His Xaa Xaa Ala Asp Gly Leu Trp Gly Pro Val
 45 50 55

```

## (2) INFORMATION FOR SEQ ID NO: 158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 8..76
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq SWWTLSSSPSEFM/IS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

```

ATTATT ATG GAA AAC TTT AAC ATG TAT AAA AAT AAG AGC TGG TGG ACC 49
Met Glu Asn Phe Asn Met Tyr Lys Asn Lys Ser Trp Trp Thr
 -20 -15 -10

CTT TTG TCC TCA TCA CCC AGC TTT ATG ATC AGT TTT GTT TCA TCT GTA 97
Leu Leu Ser Ser Ser Pro Ser Phe Met Ile Ser Phe Val Ser Ser Val
 -5 1 5

CTA CCA GTG CTA CTT ACC ATC TCT AGG TTC ATT TTG AAG CAA ATC CCA 145
Leu Pro Val Leu Leu Thr Ile Ser Arg Phe Ile Leu Lys Gln Ile Pro
 10 15 20

```

GAC CAG  
Asp Gln  
25

151

## (2) INFORMATION FOR SEQ ID NO: 159:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 142..258
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq VLAIGLLHIVLLS/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

```

AGATTCGGCC GGAGCTGCCA GCGGGGAGGC TGCAGCCGCG GGTGTGTTACA GCTGCTGGAG 60
CAGCAGCGGC CCCCGCTCCC GGGAAACCGKT CCCGGGCCGT TGRCTTCGG CCCACACGA 120
ACAGCAGAGA GGGGCAGCAG G ATG AAT GTG GGS ACA GND CAC AGC GAG GTG 171
 Met Asn Val Gly Thr Xaa His Ser Glu Val
 -35 -30

AAC CCC AAC ACG CGG GTG ATG AAC AGC CGT GGG ATC TGG CTC TCC TAC 219
Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr
 -25 -20 -15

GTG CTG GCC ATC GGT CTC CTC CAC ATC GTG CTC CTG AGC ATC CCG TTT 267
Val Leu Ala Ile Gly Leu Leu His Ile Val Leu Leu Ser Ile Pro Phe
 -10 -5 1

GTG AGT GTC CCT GTC GTC TGG ACC CTC ACC AAC CTC ATT CAC AAC ATG 315
Val Ser Val Pro Val Val Trp Thr Leu Thr Asn Leu Ile His Asn Met
 5 10 15

GGC ATG TAT ATC TTC CTG TAC ACG GTG AAG GGG ACA 351
Gly Met Tyr Ile Phe Leu Tyr Thr Val Lys Gly Thr
 20 25 30

```

## (2) INFORMATION FOR SEQ ID NO: 160:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 88..129  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.8  
seq AAASAVSVLLVAA/ER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```

AABGCTTCGT AGTGGAGGAA CGGGTTTGGC GTGTGGGACG CAGCTGCCTC TGTACTGGGG 60
AGTCACGGAG TCCCGGGCTC CAGGGAC ATG GCG GCG GCC TCT GCG GTG TCG GTG 114
 Met Ala Ala Ala Ser Ala Val Ser Val
 -10

CTG CTG GTG GCG GCG GAG AGG AAC CGG TGG CAT CGT CTC CCG AGC CTG 162
Leu Leu Val Ala Ala Glu Arg Asn Arg Trp His Arg Leu Pro Ser Leu
-5 1 5 10

CTC CTG CCG CCG AGG ACA TGG GTG TGG AGG CAA AGA ACC ATG AAG TAC 210
Leu Leu Pro Pro Arg Thr Trp Val Trp Arg Gln Arg Thr Met Lys Tyr
15 20 25

ACA ACA GCC ACA GGA AGA AAC ATG 234
Thr Thr Ala Thr Gly Arg Asn Met
30 35

```

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 177..308  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.8  
seq SGSGLSWARLSQS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

```

ACTCTTTGCC ACCCTCAGAG GCGAGCTGTG GAAGCCTTGA CTCTTAGGGC CGTTTTAGAA 60
CCGGGGCCTC GGACCGGCGG GGTTCCTGCA CGTGAACCG GAACATCTGA GATGATCGSM 120
RGGCCCTGTG GAGTGTGGGG AGCCCGGGAG TTCTTTCTTC CCTCGAGGCC CGTGCC ATG 179
 Met
GCT TAC TCC AAA GCC AGT GGG TCC CCA GTC CTA AGC CAA GCA GTC CCG 227
Ala Tyr Ser Lys Ala Ser Gly Ser Pro Val Leu Ser Gln Ala Val Pro
 -40 -35 -30

GGG GAA AAC GCT TCT CAT CCG CGT GGG AGC GCG GAT CTT GGA AGT GGC 275
Gly Glu Asn Ala Ser His Arg Arg Gly Ser Ala Asp Leu Gly Ser Gly
 -25 -20 -15

TCT GGG CTT TCT TGG GCG AGG CTC TCA CAG AGT AGA TCG GAA ATC CAT 323
Ser Gly Leu Ser Trp Ala Arg Leu Ser Gln Ser Arg Ser Glu Ile His
 -10 -5 1 5

TCT GCT GGC CCG CCC CAC CTC GGA GGA CCG ACT AAC GGA CCT GAG TTC 371
Ser Ala Gly Pro Pro His Leu Gly Gly Arg Thr Asn Gly Pro Glu Phe
 10 15 20

CCG GCC CTA TCT TAC TCT TCT CAG CTT CTC AGC TTG GCT CAG CTC AGA 419
Pro Ala Leu Ser Tyr Ser Ser Gln Leu Leu Ser Leu Ala Gln Leu Arg
 25 30 35

GGA AGA GGA ATC ACT GAA GTC TCA GAG AAG TCT CCA CTC ATC 461
Gly Arg Gly Ile Thr Glu Val Ser Glu Lys Ser Pro Leu Ile
 40 45 50

```

## (2) INFORMATION FOR SEQ ID NO: 162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 175..285
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq RPVLLHLHQTAHA/DE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

```

AGGCTCCGCG CTCTGGAGGC TCAGGCGCCG CGTGGGGCCC GCACCTCTGG GCAGCAGCGG 60

```



CAGCCGAGAC TCACGGTCAA GCTAAGSCSA AGASTGGCTG GCTGAAGCCA TACTATTTTA 120  
 TAGAATTAAT GGRAARCMHG AAAAGMCATC ACAAAACCAAG AAGAACTTTG GAAA ATG 177  
 Met  
 AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG 225  
 Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr  
 -35 -30 -25  
 GGA GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA 273  
 Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln  
 -20 -15 -10 -5  
 ACA GCC CAT GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA 321  
 Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr  
 1 5 10  
 CAG GAA CTC TTT CCA CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT 369  
 Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile  
 15 20 25  
 ATA GCA TCT CTG ACT TTT CTT TAC ACT CTT CTG AGC GAA GTA ATT CAC 417  
 Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His  
 30 35 40  
 CCT TTA GCA ACT TCC CAT CAA CAA TAT TTT TAT AAA ATT CAA 459  
 Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Gln  
 45 50 55

## (2) INFORMATION FOR SEQ ID NO: 163:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 25..81
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq IPCAHMLVCPTIG/DI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

AATTTGTAAG AATATTATAT ATAG ATG ATC ATC TGT TAT GAT ATT CCT TGT 51  
 Met Ile Ile Cys Tyr Asp Ile Pro Cys  
 -15  
 GCA CAT ATG TTG GTT TGT CCT ACT ATT CGT GAT ATT AAG TTT GAT CAC 99  
 Ala His Met Leu Val Cys Pro Thr Ile Gly Asp Ile Lys Phe Asp His

|                                                         |    |    |   |     |
|---------------------------------------------------------|----|----|---|-----|
| -10                                                     | -5 | 1  | 5 |     |
| TTG ATG AAG TGG TAT CCA TCA GAT TTC TCT ACT GAA AGG CTG |    |    |   | 141 |
| Leu Met Lys Trp Tyr Pro Ser Asp Phe Ser Thr Glu Arg Leu |    |    |   |     |
| 10                                                      | 15 | 20 |   |     |

## (2) INFORMATION FOR SEQ ID NO: 164:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 184..240
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq STLASVPPAATFG/AD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| AACCAGGCTC TATTTAGAGC CGGGTAGGGG AGCGCAGGNC CAGATACCTC ASCGCTACCT   | 60  |
| GGCGGAAGCTG GATTTCTCTC CCGCCTGCCG GCCTGCCCTGC CACAGCCGGA CTCCGCCACT | 120 |
| CCGGTAGCCC CATGGCTGGM AACCTGTGAG ATTAGCAATA TTTTAGCAA CTACTTCAGT    | 180 |
| GCG ATG TAC AGC TCG GAG GAC TCC ACC CTG GCC TCT GTT CCC CCT GCT     | 228 |
| Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val Pro Pro Ala         |     |
| -15 -10 -5                                                          |     |
| GCC ACC TTT GGS GCC GAT GAC TTG GTA CTG ACC CTG AGC AAC CCC CAG     | 276 |
| Ala Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln     |     |
| 1 5 10                                                              |     |
| ATG TCA TTG GAG GGT ACA GAG AAG GCC AGC TGG TTG GGG GAA CAG CCC     | 324 |
| Met Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro     |     |
| 15 20 25                                                            |     |
| CAG TTC TGG TCG AAG ACG CAG GTT CTG GAC TGG ATC AGC TAC CAA GTG     | 372 |
| Gln Phe Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val     |     |
| 30 35 40                                                            |     |
| GAG AAG AAC AAG TAC GAC GCG                                         | 393 |
| Glu Lys Asn Lys Tyr Asp Ala                                         |     |
| 45 50                                                               |     |

## (2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 263 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 54..248  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq QLEGLNWLRFSSWA/QG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

```

ACCCTGAATA CGAAGAACAT AAGCAAAGCT ACTGGAGACA CCGAGAACTA ATT ATG 56
 Met
 -65

GGG GAA GAC CCT KCC CAG CCC CGC AAG TAT AAG AAG WWG AAG AWG GAG 104
Gly Glu Asp Pro Xaa Gln Pro Arg Lys Tyr Lys Lys Xaa Lys Xaa Glu
 -60 -55 -50

CTA CAG GGT GAT KGG CCT CCC AGT TCT CCC ACT AAT GAT CCT ACC GTG 152
Leu Gln Gly Asp Xaa Pro Pro Ser Ser Pro Thr Asn Asp Pro Thr Val
 -45 -40 -35

AAA TAT GAG ACT CAG CCA CGG TTT ATC ACA GCC ACT GGA GGC ACC CTG 200
Lys Tyr Glu Thr Gln Pro Arg Phe Ile Thr Ala Thr Gly Gly Thr Leu
 -30 -25 -20

CAC ATG TAT CAG TTG GAA GGG CTG AAC TGG CTA CGC TTC TCC TGG GCC 248
His Met Tyr Gln Leu Glu Gly Leu Asn Trp Leu Arg Phe Ser Trp Ala
 -15 -10 -5

CAG GGC ACT KWC GGG
Gln Gly Thr Xaa Gly
 1 5

```

(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 372 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 148..273  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq LLGCLQCCWLQSG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

```

ACCAATTTTG TAGTTATCTG ATCTGAAGGA AGATGTGTGT GGAGGTGTTT AGTGATGTTT 60
TCCSATGACG GTGATTCGCC CTAAATCTAC GTATTAAATA CAATGGAACA GSATCCACAG 120
TTCACCCCTA ATAATATAGT TTACTGA ATG TTT TAT GTA GCT ATG ACC AAA ACT 174
 Met Phe Tyr Val Ala Met Thr Lys Thr
 -40 -35

CAC AAA AGG ATC AGA AGC CTC TGT AAC ATC CAC CAT GGT TTG TTC CAG 222
His Lys Arg Ile Arg Ser Leu Cys Asn Ile His His Gly Leu Phe Gln
 -30 -25 -20

TTT ACT CAG CAG CTC CTG GGC TGT CTT CAG TGC TGT TGG CTG CAA TCA 270
Phe Thr Gln Gln Leu Leu Gly Cys Leu Gln Cys Cys Trp Leu Gln Ser
 -15 -10 -5

GGC AGA GCC CCA GCT ACC TAT TAC CTT GTG GAG AGT ATT GAA AAG TCA 318
Gly Arg Ala Pro Ala Thr Tyr Tyr Leu Val Glu Ser Ile Glu Lys Ser
 1 5 10 15

GCA CAT GGC TCT GTA TTA NGT ACT TAT GAT CAA ACT CAG ACT CGC ATA 366
Ala His Gly Ser Val Leu Xaa Thr Tyr Asp Gln Thr Gln Thr Arg Ile
 20 25 30

GGC AGG 372
Gly Arg

```

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 158..337  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq XTCASXNP3QCLA/AF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

```

ACAGAATCTT TAGGTGGGCC TGTGGT3AG GTCACCTTTTC CCTAATCGTA TATTCCAGTT 60
CCTGTAGATC CTATTCCAGT TCCCAGGACA TATTCCAACC TCGACCTCCA GCCAACTTTG 120
AAGCCCTGAA GTTGTGTGCT GATGTGTTTC TAACAAC ATG GTC TCA CCC AAA GAT 175
 Met Val Ser Pro Lys Asp
 -60 -55
CTT CCT CTT GTG CTT TTG CAG GAC ATT AAA GTT CCC AGC TCC ATG ACT 223
Leu Pro Leu Val Leu Leu Gln Asp Ile Lys Val Pro Ser Ser Met Thr
 -50 -45 -40
GGA TCA CAT GCT GGA AAC CCT CAT ATA GAA AGG AAT GAT CTC CCC AGA 271
Gly Ser His Ala Gly Asn Pro His Ile Glu Arg Asn Asp Leu Pro Arg
 -35 -30 -25
CAT GGT TCT CCT CAA TTT TTT ACA GGH HYG ACT TGT GCT TCT RCA AAC 319
His Gly Ser Pro Gln Phe Phe Thr Gly Xaa Thr Cys Ala Ser Xaa Asn
 -20 -15 -10
CCA TCT CAG TGT CTG GCA GCA TTT 343
Pro Ser Gln Cys Leu Ala Ala Phe
 -5 1

```

## (2) INFORMATION FOR SEQ ID NO: 168:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 1..45
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq FXSLFCLYFSCFL/HI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

```

ATG GAA TTT KTT TCT CTT TTC TGT CTC TAC TTC AGC TGT TTC CTA CAT 48
Met Glu Phe Xaa Ser Leu Phe Cys Leu Tyr Phe Ser Cys Phe Leu His
-15 -10 -5 1
ATT ATA TAT TTT KKC AGC TGT TTC CTA TAC 73
Ile Ile Tyr Phe Xaa Ser Cys Phe Leu Tyr
5 10

```

## (2) INFORMATION FOR SEQ ID NO: 169:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 10..144
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq ALLELIDSPECLS/KC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

```

ACTGGGAAG ATG GCG CTG CAC TTC CAG AGT TTG GCT GAA TTG GAA RTG TTA 51
 Met Ala Leu His Phe Gln Ser Leu Ala Glu Leu Glu Xaa Leu
 -45 -40 -35

TGT ACT CAT CTC TAC ATA GGG ACT GAT CTT ACA CAA AGA ATA GAG GCT 99
 Cys Thr His Leu Tyr Ile Gly Thr Asp Leu Thr Gln Arg Ile Glu Ala
 -30 -25 -20

GAG AAA GCA CTC TTG GAA CTT ATT GAC AGT CCA GAA TGT CTC AGC AAG 147
 Glu Lys Ala Leu Leu Glu Leu Ile Asp Ser Pro Glu Cys Leu Ser Lys
 -15 -10 -5 1

TGT CAA CTT TTA TTA GAA CAA GGA ACA ACA TCC TAT GCT CAG CTC CTT 195
 Cys Gln Leu Leu Leu Glu Gln Gly Thr Thr Ser Tyr Ala Gln Leu Leu
 - 5 10 15

GCA GCA ACC GKV 207
 Ala Ala Thr Xaa
 20

```

## (2) INFORMATION FOR SEQ ID NO: 170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 299..379
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq LLLLLITPSPSPL/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

```

ACCTTGGGCT CCAAATTCTA GCTCATAAAG ATGCAAGTKT TGCAATTTCG TATAAATGCT 60
TAAGAAAAGA GCAAGCTGTC CAGAGAGTGA GAAGTTTGAA AAGAGAGGCT CATAAGAGAG 120
AAATGATGTC CATTTGAGCC CCACCACGGA GGTTATGTGG TCCCAAAAGG AATGATGGCC 180
AAGCAATTAA TTTTCCTCC TAGTTCTTAG CTIGCTTCTG CATTGATTGG CTTTACACAA 240
CTGGCATTTA GTCTGCATTA CACAAATAGA CACTAATTTA TTTGGAACAA GCAGCAAA 298
ATG AGA ACT TTA TTT GGT GCA GTC AGG GCT CCA TTT AGT TCC CTC ACT 346
Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
 -25 -20 -15

CTG CTT CTA ATC ACC CCT TCT CCC AGC CCT CTT CTA TTT GAT AGA GGT 394
Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
 -10 -5 1 5

CTG TCC CTC AGA TCA GCA ATG TCG 418
Leu Ser Leu Arg Ser Ala Met Ser
 10

```

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 107..229
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq AVSSLIAVGTSHG/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

```

ACACTCCTAT GATACTTCAT CTGTGGCAAG CTCAGATAGT GSTGACAGGA CCAACTTAAA 60

```

AAGGAAGAAG AAATTACCTG ATTCTTTTTC ACTTCATGGA TCAGTT ATG CCG CAT 115  
Met Arg His  
-40

TCA CTT TTG AAG GGA ATT TCT GCC CAG ATA GTG TCT GCA GGT GAC AAA 163  
Ser Leu Leu Lys Gly Ile Ser Ala Gln Ile Val Ser Ala Ala Asp Lys  
-35 -30 -25

GTA GAT GCT GGC TTG CCT ACA GCA ATT GCA GTA TCC AGT CTG ATA GCA 211  
Val Asp Ala Gly Leu Pro Thr Ala Ile Ala Val Ser Ser Leu Ile Ala  
-20 -15 -10

GTG GGT ACA TCT CAT GGA TTG GCT GGG 238  
Val Gly Thr Ser His Gly Leu Ala Gly  
-5 1

## (2) INFORMATION FOR SEQ ID NO: 172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 120..164
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq LSCFIFFYISSLC/CF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

TGTGAAGATG ACAGAGATCT AACTTCTGAG AGCAGAGGTG TCAAGTGACG GTCCCCCTTGG 60

AGGAATGGTC TTTCATCTG ACTACTTCCT TCTGCAACTG TGTTCTTCCA TTAGCTTCC 119

ATG ACA CTC TCC TGC TTT ATT TTT TTC TAC ATC TCT AGC CTT TGC TGT 167  
Met Thr Leu Ser Cys Phe Ile Phe Phe Tyr Ile Ser Ser Leu Cys Cys  
-15 -10 -5 1

TTC CTC TCC TAC CCC ACC AGG 188  
Phe Leu Ser Tyr Pro Thr Arg  
5

## (2) INFORMATION FOR SEQ ID NO: 173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs



(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 28..72  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq LCFLLPHRLQEA/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

```
ATAGATCAGT GACGTCTTTT TCTTCAG ATG ATC CTA TGT TTC CTT CTT CCT CAT 54
 Met Ile Leu Cys Phe Leu Leu Pro His
 -15 -10

CAT CGT CTT CAG GAA GCC AGA CAG ATT CAA GTA TTG AAG ATG CTG CCA 102
His Arg Leu Gln Glu Ala Arg Gln Ile Gln Val Leu Lys Met Leu Pro
 -5 1 5 10

AGG GAA AAA TTA AGR AGA AGR AGA AGA GAG AAA ACA AAT AAA TGG GAA 150
Arg Glu Lys Leu Arg Arg Arg Arg Arg Glu Lys Thr Asn Lys Trp Glu
 15 20 25

AAA AGA AAG GGC AGC GGG 168
Lys Arg Lys Gly Ser Gly
 30
```

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOJBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 64..105  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq FSLFALNMPLGFC/VY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

```

TTTATTTTAA CCATCTTTTA CTATTTTATG AAGGAACTA GCTTAGTAG TGGGTGCCC 60
TGT ATG TTT TCT CTT TTT GCT CTT AAT ATG CCA TTG GGT TTT TGT GTG 108
Met Phe Ser Leu Phe Ala Leu Asn Met Pro Leu Gly Phe Cys Val
 -10 -5 1

TAT GTG ATT TTC AAA ATT CAT GAC TGG 135
Tyr Val Ile Phe Lys Ile His Asp Trp
 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 163..255
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq SVWGVLPSPACSA/DL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

```

ATTTGATTTT AGTCAGGGTG TAAGAATATG TATTATTGTT CCCAAAAAAA TCTGTGTAAA 60
AACTTCATAG TGTGAAACAG TGGCAACTGS KTGATTAAAA CATCATTTAG AAAAGACACT 120
CTTCCCTGTT TTGAAATTGA CTCCTCAAAA GGACAGCTGA AC ATG GCC TCT TCT 174
Met Ala Ser Ser
 -30

CCA GGT GTC GCC ATG CAC TCC CTC TGG GCC ACC ATA CAC ACT TCT GTG 222
Pro Gly Val Ala Met His Ser Leu Trp Ala Thr Ile His Thr Ser Val
 -25 -20 -15

TGG GGC GTG CTC CCA CCT CCA GCC TGC TCA GCT GAT CTT TTG TTC AGC 270
Trp Gly Val Leu Pro Pro Pro Ala Cys Ser Ala Asp Leu Leu Phe Ser
 -10 -5 1 5

AAT GCC TGT CTA CTT CCC CAT GAG ATC CAC CTG 303
Asn Ala Cys Leu Leu Pro His Glu Ile His Leu
 10 15

```

## (2) INFORMATION FOR SEQ ID NO: 176:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 60..194
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq LPRLLSLSQHSSES/WI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

```

AGAGTTTCCG GTCTGGGCTT TGGCGGGTCT GGTTTGAAGC TCTCCTGTTT GACGAAAGT 59
ATG TCT CAG GAA GGT GCG GTC CCA GCT AGC GCG GTT CCC CTG GAA GAA 107
Met Ser Gln Glu Gly Ala Val Pro Ala Ser Ala Val Pro Leu Glu Glu
-45 -40 -35 -30

TTA AGT AGC TGG CCA GAG GAG CTA TGC CGC CGG GAA CTG CCG TCC GTC 155
Leu Ser Ser Trp Pro Glu Glu Leu Cys Arg Arg Glu Leu Pro Ser Val
 -25 -20 -15

CTG CCC CGA CTC CTC TCA TTG TCT CAA CAT TCT GAA AGT TGG ATT GAG 203
Leu Pro Arg Leu Leu Ser Leu Ser Gln His Ser Glu Ser Trp Ile Glu
 -10 -5 1

CAT ATT CAA ATT TTG AAA ATT ATT GTA GAA ATG TTT TTA CCT CAT ATG 251
His Ile Gln Ile Leu Lys Ile Ile Val Glu Met Phe Leu Pro His Met
 5 10 15

AAC CAC CTG ACA TTG GAA CAG ACT TTC TTT TCA CAA GTG TTA CCA AAG 299
Asn His Leu Thr Leu Glu Gln Thr Phe Phe Ser Gln Val Leu Pro Lys
 20 25 30 35

ACT GTG AAA TTA TTC GAT
Thr Val Lys Leu Phe Asp
 40

```

## (2) INFORMATION FOR SEQ ID NO: 177:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 254..361  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq AAVVFAVVLSIHA/TV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

```
AGTAACTGTG AGGAAGGCTG CAGAGTGGCG ACGTCTACGC CGTAGGTTGS AGGCTGTGGG 60
GGGTGGCCCG GGGCCAGGTC CCAGGCCGCA GAAGTGACCT GCGGTGGAST TCCCTCCTCG 120
CTGCTGGAGA ACGGAAGGGA ARAAGGTTSC TGGCCGGGTG AAAGTGCCCTC CCTCTGCTTG 180
ACGGGGCTGA GGGGCCCCGAA GTCTAGGGCG TCCGTAGTCG CCCCAGCCTC CGTGAAGCCC 240
CAGGTCTAGA GAT ATG ACC CGA GAG TGC CCA TCT CCG GCC CCG GGG CCT 289
 Met Thr Arg Glu Cys Pro Ser Pro Ala Pro Gly Pro
 -35 -30 -25

GGG GCT CCG CTG AGT GGA TCG GTG CTG GCA GAG GCG GCA GTA GTG TTT 337
Gly Ala Pro Leu Ser Gly Ser Val Leu Ala Glu Ala Ala Val Val Phe
 -20 -15 -10

GCA GTG GTG CTG AGC ATC CAC GCA ACC GTA TGG 370
Ala Val Val Leu Ser Ile His Ala Thr Val Trp
 -5 1
```

## (2) INFORMATION FOR SEQ ID NO: 178:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 369..470  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 2..103  
id AA059664  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 216..263

(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 14.8  
 seq LLWWALLLLGLAQA/CP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

```

AAGTGGATGG TTCCAGGCAC CCTGTCTGGC GCAGGGAGGG CACAGGCGTG CACATCGAAG 10
GTGGGGGTGGC ACCAGGCTCC CCCTCGCCCC AGCATCCAAG TCCTCCCTTG GGC3CCCCGTG 120
GCCCTGGCAG ACTCTCAGGG STAAGGTCCT CTGTTGCTTT TTGGTTCCAC CTTAGAAGAG 180
GCTCGCTTGA CTAAGASTAG CTTGAAGGAG GCACC ATG CAG GAG CTG CAT CTG 233
 Met Gln Glu Leu His Leu
 -15

CTC TGG TGG GCG CTT CTC CTG GGC CTG GCT CAG GCC TGC CCT GAG CCC 281
Leu Trp Trp Ala Leu Leu Leu Gly Leu Ala Gln Ala Cys Pro Glu Pro
-10 -5 1

TGC GAC TGT GGG GAA AAG TAT GGC TTC CAG ATC GCC GAC TGT GCC TAC 329
Cys Asp Cys Gly Glu Lys Tyr Gly Phe Gln Ile Ala Asp Cys Ala Tyr
5 10 15 20

CGC GAC CTA GAA TCC GTG CCG CCT GGC TTC CCG GCC AAT GTG ACT ACA 377
Arg Asp Leu Glu Ser Val Pro Pro Gly Phe Pro Ala Asn Val Thr Thr
25 30 35

CTG AGC CTG TCA GCC AAC CGG CTG CCA GGC TTG CCG GAR GGT GCC TTC 425
Leu Ser Leu Ser Ala Asn Arg Leu Pro Gly Leu Pro Glu Gly Ala Phe
40 45 50

AGG GAG GTG CCC CTG CTG CAG TCG CTG TGG CTG GCA CAC AAT GAG 470
Arg Glu Val Pro Leu Leu Gln Ser Leu Trp Leu Ala His Asn Glu
55 60 65

```

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 69..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
 region 1..260  
 id H96534  
 est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 14..67
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.6  
seq LLLALCATGAQG/LY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```

CTCTCTGCGG GCG ATG GGG CGG CAG GCC CTG CTG CTT CTC GCG CTG TGC 49
 Met Gly Arg Gln Ala Leu Leu Leu Leu Ala Leu Cys
 -15 -10

GCC ACA GGC GGC CAG GGG CTC TAC TTC CAC ATC GGC GAG ACC GAG AAG 97
Ala Thr Gly Ala Gln Gly Leu Tyr Phe His Ile Gly Glu Thr Glu Lys
 -5 1 5 10

CGC TGT TTC ATC GAG GAA ATC CCC GAC GAG ACC ATG GTC ATC GGC AAC 145
Arg Cys Phe Ile Glu Glu Ile Pro Asp Glu Thr Met Val Ile Gly Asn
 15 20 25

TAT CGT ACC CAG ATG TGG GAT AAG CAG AAG GAG GTC TTC CTG CCC TCG 193
Tyr Arg Thr Gln Met Trp Asp Lys Gln Lys Glu Val Phe Leu Pro Ser
 30 35 40

ACC CCT GGC CTG GGC ATG CAC GTG GAA GTG AAG GAC CCC GAC GGC AAG 241
Thr Pro Gly Leu Gly Met His Val Glu Val Lys Asp Pro Asp Gly Lys
 45 50 55

GTG GTG CTG TCC CGG CAG TAC GGC TCG GAG GGC CGC TTC ACG TTC ACC 289
Val Val Leu Ser Arg Gln Tyr Gly Ser Glu Gly Arg Phe Thr Phe Thr
 60 65 70

TCC CAC ABN KSG GGT GAC CAT CAA ATC TGT CTG CAC TGC GGG 331
Ser His Xaa Xaa Gly Asp His Gln Ile Cys Leu His Cys Gly
 75 80 85

```

## (2) INFORMATION FOR SEQ ID NO: 180:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..129
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..40

id AA134726  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 157..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 66..104  
id AA134726  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 124..156  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 34..66  
id AA134726  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 107..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..89  
id R17226  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 76..138  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 12.7  
seq ILFLLSWSGPLQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

```
AAGCTAACCC TCGGGCTTGA GGGGAAGAGG CTGACTGTAC GTTCCTTCTA CTCTGGCACC 60
ACTCTCCAGG CTGCC ATG GGG CCC AGC ACC CCT CTC CTC ATC TTG TTC CTT 111
 Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu
 -20 -15 -10

TTG TCA TGG TCG GGA CCC CTC CAA GGA CAG CAG CAC CAC CTT GTG GAG 159
Leu Ser Trp Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu
 -5 1 5

TAC ATG GAA CGC CGA CTA GCT GCT TTA GAG GAA CGG 195
Tyr Met Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg
 10 15
```

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 base pairs  
(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 313..349  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 7..43  
id T67245  
est

(ix) FEATURE:

(A) NAME/KEY: sig peptide  
(B) LOCATION: 119..199  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.8  
seq LLLLCPLSRGCCP/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

```

ACGTTACCTT TGGGTGGTGG TTTTCATGCC TGTGCCGCCT GCTTCTGGGC CAGTGATCCA 60
GGTGTCTGGT GACCACCCGG GCACAGCTGC TTGGCTGCTG TGGGCACCTC AGCTTCCC 118
ATG TCC TGT AGG GAA CTC ACC CAC CGG CCT TGC TCT CCA CAC CTC TTA 166
Met Ser Cys Arg Glu Leu Thr His Arg Pro Cys Ser Pro His Leu Leu
 -25 -20 -15
CTC CTG TGT CCC CTT TCT CGG GGA TGC TGC CCC CTC CTG CTG TCC KGT 214
Leu Leu Cys Pro Leu Ser Arg Gly Cys Cys Pro Leu Leu Leu Ser Xaa
 -10 -5 1 5
CCY CTG TWA GGG GTG AAT CTT GAA TCC ATC TTA TCT CTT ACT CTC CCT 262
Pro Leu Xaa Gly Val Asn Leu Glu Ser Ile Leu Ser Leu Thr Leu Pro
 10 15 20
CCC TCT CCC AGC TCA GTC GGG CTC TCA CCC TCT GTG ACC CAS CTC ACA 310
Pro Ser Pro Ser Ser Val Gly Leu Ser Pro Ser Val Thr Xaa Leu Thr
 25 30 35
ACT TCA CCT GTT TCA TTG CAC TTT GCA TCC GMC CTC GCC GGG 352
Thr Ser Pro Val Ser Leu His Phe Ala Ser Xaa Leu Ala Gly
 40 45 50

```

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prestate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 113..306

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 71..264  
id H83784  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 42..111

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 1..70  
id H83784  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 378..414

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94  
region 346..382  
id H83784  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 305..340

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94  
region 264..299  
id H83784  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 250..350

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96  
region 2..102  
id W32197  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 392..449

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 142..199  
id W32197  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 349..390  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 100..141  
id W32197  
est

(ix) FEATURE:

[illegible]

(ix) FEATURE:

```
(A) NAME/KEY: sig_peptide
(B) LOCATION: 85..150
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.5
 seq AALLLGGLMMVVIG/DE
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

|             |                 |                 |                     |                     |             |    |
|-------------|-----------------|-----------------|---------------------|---------------------|-------------|----|
| AACTTGTGTC  | CGGGTGGWRG      | ACTGGATTAG      | CTGCGGASCC          | TGGAAGCTGC          | CTGTCCCTTCT | 60 |
| CCCTGTGCTT  | AACCAGAGGT      | GCCC            | ATG GGT TGG ACA     | ATG AGG CTG GTC ACA | 111         |    |
|             |                 |                 | Met Gly Trp Thr     | Met Arg Leu Val Thr |             |    |
|             |                 |                 | -20                 | -15                 |             |    |
| GCA GCA CTG | TTA CTG GGT CTC | ATG ATG GTG GTC | ACT GGA GAC GAG GAT | 159                 |             |    |
| Ala Ala Leu | Leu Leu Gly Leu | Met Met Val Val | Thr Gly Asp Glu Asp |                     |             |    |
|             | -10             | -5              | 1                   |                     |             |    |
| GAG AAC AGC | CCG TGT GCC CAT | GAG GCC CTC TTG | GAC GAG GAC ACC CTC | 207                 |             |    |
| Glu Asn Ser | Pro Cys Ala His | Glu Ala Leu Leu | Asp Glu Asp Thr Leu |                     |             |    |
| 5           | 10              | 15              |                     |                     |             |    |
| TTT TGC CAG | GGC CTT GAA GTT | TTC TAC CCA GAG | TTG GGG AAC ATT GGC | 255                 |             |    |
| Phe Cys Gln | Gly Leu Glu Val | Phe Tyr Pro Glu | Leu Gly Asn Ile Gly |                     |             |    |
| 20          | 25              | 30              | 35                  |                     |             |    |
| TGC AAG GTT | GTT CCT GAT TGT | DAC AAC TAC AGA | CAG AAG ATC ACC TCC | 303                 |             |    |
| Cys Lys Val | Val Pro Asp Cys | Xaa Asn Tyr Arg | Gln Lys Ile Thr Ser |                     |             |    |
|             | 40              | 45              | 50                  |                     |             |    |
| TGG ATG GAG | CCG ATA GTC AAG | TTC CCG GGG GCC | GTG GAC GGC GCA ACC | 351                 |             |    |
| Trp Met Glu | Pro Ile Val Lys | Phe Pro Gly Ala | Val Asp Gly Ala Thr |                     |             |    |
|             | 55              | 60              | 65                  |                     |             |    |
| TAT ATC CTG | GTG ATG GTG GAT | CCA GAT GCC CCT | AGC AGA GCA GAA CCC | 399                 |             |    |
| Tyr Ile Leu | Val Met Val Asp | Pro Asp Ala Pro | Ser Arg Ala Glu Pro |                     |             |    |
|             | 70              | 75              | 80                  |                     |             |    |
| AGA CAG AGA | TTC TGG AGA CAT | TGG CTG GTA ACA | GAT ATC AAG GGG GCC | 447                 |             |    |
| Arg Gln Arg | Phe Trp Arg His | Trp Leu Val Thr | Asp Ile Lys Gly Ala |                     |             |    |
| 85          | 90              | 95              |                     |                     |             |    |

## (2) INFORMATION FOR SEQ ID NO: 183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..182
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 6..63  
id R18560  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 176..213
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 58..95  
id R18560  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..182
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..38  
id R13864  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 176..213
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 33..70  
id R13864  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 176..213
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 2..39  
id HSC01E071  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 113..190
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3  
seq VHLLSLCSGKVYA/RM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

```

ACTGGGAGCC GCCTCCGTCG CCGCCSTCAG AGCCGCCCTA TCAGAGTTCC TACCANTTTG 60
TGSTCCAGC AGCTTCTGTT CCAGATTATC TTAACAAGAA AACCAACTGG AAAAAAAAAA 118
ATG AAA TTC CTT ATC TTC GCA TTT TTC GGT GGT GTT CAC CTT TTA TCC 168
Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser
 -20 -15 -10
CTG TGC TCT GGG AAA GTA TAT GCA AGA ATG GCA TCT CTA AGA GGA CTC 214
Leu Cys Ser Gly Lys Val Tyr Ala Arg Met Ala Ser Leu Arg Gly Leu
 -5 1 5
GGG
Gly
217

```

## (2) INFORMATION FOR SEQ ID NO: 184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 139..361
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 92..314  
id AA100852  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..434
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 314..388  
id AA100852  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 139..434  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 100..395  
id AA224847  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 139..361  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 92..314  
id AA161042  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 368..434  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 323..389  
id AA161042  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 139..365  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 87..313  
id H64488  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 52..144  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 1..93  
id H64488  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 171..396  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 129..354  
id AA088770  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 167..253  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.1  
seq LIFLCGAALLAVG/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

```

AAAAAGCGCC TACCCTGCCCT GCAGGTGAGC AGTGGTGTGT GAGAGCCAGG CGTCCCTCTG 60
CCTGCCCCACT CAGTGGCAAC ACCCGGGAGC TGTTTTGTCC TTTGTGGAGC CTCAGCAGTT 120
CCCTCTTTCA GAACTYRVYK GCCAAGAGCC CTGAACAGGA GCCACC ATG CAG TGC 175
 Met Gln Cys
TTC AGC TTC ATT AAG ACC ATG ATG ATC CTC TTC AAT TTG CTC ATC TTT 223
Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu Leu Ile Phe
-25 -20 -15
CTG TGT GGT GCA GCC CTG TTG GCA GTG GGC ATC TGG GTG TCA ATC GAT 271
Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val Ser Ile Asp
-10 -5 1 5
GGG GCA TCC TTT CTG AAG ATC TTC GGG CCA CTG TCG TCC AGT GCC ATG 319
Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser Ser Ala Met
 10 15 20
CAG TTT GTC AAC GTG GGC TAC TTC CTC ATC GCA GCC GGC GTT GTG GTC 367
Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly Val Val Val
 25 30 35
TTT GCT CTT GGT TTC CTG GGC TGC TAT GGT GCT AAG ACT GAG AGC AAG 415
Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr Glu Ser Lys
 40 45 50
TGT GCC CTC GTG ACG TTC 433
Cys Ala Leu Val Thr Phe
55 60

```

## (2) INFORMATION FOR SEQ ID NO: 185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..242
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 1..115  
id R58075  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 220..303

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.6  
seq IVSLLGFVATVTL/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

```

AAGATAAGCG GGTGCAGCGG GGCAGAACAT AGGTTCCTT AGAGAGGTTT CCGGAGTCC 60
CGACGGCGGC TCAAGTCAGA GTTGCTGGGT TTTGCTCAGA TTGGTGTGGG AAGAGCCTGC 120
CTGTGGGGAG CGGCCACTCC ATACTGCTGA GGGCTCAGGA CTGCTGCTCA GCTTGCCCGT 180
TACCTGAAGA GCGGCGGGAS GGGCCCCTGA GGGGTCACC ATG TGG GCC TTC TCG 234
 Met Trp Ala Phe Ser
 -25

GAA TTG CCC ATG CCG CTG CTG ATC AAT TTG ATC GTC TCG CTG CTG GGA 282
Glu Leu Pro Met Pro Leu Leu Ile Asn Leu Ile Val Ser Leu Leu Gly
 -20 -15 -10

TTT GTG GCC ACA GTC ACC CTC ATC CCG GCC TTC CGG GGC CAC TTC ATT 330
Phe Val Ala Thr Val Thr Leu Ile Pro Ala Phe Arg Gly His Phe Ile
 -5 1 5

GCT GCG CGC CTC TGT GGT CAG GAC CTC AAC AAA ACC AGC CAG 372
Ala Ala Arg Leu Cys Gly Gln Asp Leu Asn Lys Thr Ser Gln
 10 15 20

```

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..403
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 33..324  
id H97426  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 59..295
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 2..239  
id W44834

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 106..156  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 4..54  
 id R57989  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 161..190  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 62..91  
 id R57989  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 148..204  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.3  
 seq VLMRLVASAYSIA/QK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

```

AGCTGAGGTA GGGATGCSAT CCTTCTCAAA AGACTTATTG ACAGTGCCAA AGCTSGGTAC 60
TGGACACAAC GAGGCACCTG GGTCTACGAT AACGCGCTTK TGCTCCTCCT GAAGTGTCTT 120
TGGTCCAACG TTGTTCCAGA GTGTACC ATG GCT TCC AGT AAC ACT GTG TTG ATG 174
 Met Ala Ser Ser Asn Thr Val Leu Met
 -15

CGG TTG GTA GCC TCC GCA TAT TCT ATT GCT CAA AAG GCA GGD ATG ATA 222
Arg Leu Val Ala Ser Ala Tyr Ser Ile Ala Gln Lys Ala Gly Met Ile
-10 -5 1 5

GTC AGA CGT GTT ATT GCT GAA GGA GAC CTG GGT ATT GTG GAG ADG ACC 270
Val Arg Arg Val Ile Ala Glu Gly Asp Leu Gly Ile Val Glu Xaa Thr
 10 15 20

TGT GCA ACA GAC CTG CAG ACC AAA GCT GAC CGA TTG GCA CAG ATG AGN 318
Cys Ala Thr Asp Leu Gln Thr Lys Ala Asp Arg Leu Ala Gln Met Xaa
 25 30 35

ATA TGT TCT TCA TTG GCC CGG AAA TTC CCC AAA CTC ACA ATT ATA GGG 366
Ile Cys Ser Ser Leu Ala Arg Lys Phe Pro Lys Leu Thr Ile Ile Gly
 40 45 50

GAA GAG GAT CTG CCT TCT RMG GAA GTG GAT CAA GAG 402
Glu Glu Asp Leu Pro Ser Xaa Glu Val Asp Gln Glu
 55 60 65

```

## (12) INFORMATION FOR SEQ ID NO: 187:



- (1) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 317 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: DOUBLE  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 111..318  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 6..213  
                            id R18560  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 131..318  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 1..188  
                            id R13864  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 162..318  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 1..157  
                            id HSC01E071  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 207..318  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 1..112  
                            id AA016124  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: 105..176  
    (C) IDENTIFICATION METHOD: Von Haighe matrix  
    (D) OTHER INFORMATION: score 5.9  
                            seq VHLLSLCSGKAIC/KN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

AAGTAAGGCT AGGYCGCGAG CTTAGTCCTG GGAGCCGCCT CGGTGCGCGC CGTCAGAGCC 60

```

GCCCTATCAG ATTATCTTAA CAAGAAAACC AACTGGAAAA AAAA ATG AAA TTC CTT 116
 Met Lys Phe Leu

ATC TTC GCA TTT TTC GGT GGT GTT CAC CTT TTA TCC CTG TGC TCT GGG 164
Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser Leu Cys Ser Gly
-20 -15 -10 -5

AAA GCT ATA TGC AAG AAT GGC ATC TCT AAG AGG ACT TTT GAA GAA ATA 212
Lys Ala Ile Cys Lys Asn Gly Ile Ser Lys Arg Thr Phe Glu Glu Ile
 1 5 10

AAA GAA GAA ATA GCC AGC TGT GGA GAT GTT GCT AAA GCA ATC ATC AAC 260
Lys Glu Glu Ile Ala Ser Cys Gly Asp Val Ala Lys Ala Ile Ile Asn
 15 20 25

CTA GCT GTT TAT GGT AAA GCC CAG AAC AGA TCC TAT GGC CGA TTG GCA 308
Leu Ala Val Tyr Gly Lys Ala Gln Asn Arg Ser Tyr Xaa Arg Leu Ala
 30 35 40

CTT CTG GTT 317
Leu Leu Val
45

```

## (2) INFORMATION FOR SEQ ID NO: 188:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..401
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 59..300  
id H29377  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 454..499
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 356..401  
id H29377  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..179
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95  
region 36..79  
id H29377  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 397..436  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 297..336  
id H29377  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 135..295  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 293..453  
id N28905  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 45..127  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 4..86  
id N28905  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 334..388  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 489..543  
id N28905  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 135..395  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 81..341  
id H11885  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 160..334  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 105..329  
id H15231  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 136..181  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 82..127  
 id H15231  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 146..298  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.9  
 seq ALXVLP LLGLHEA/AS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```

AACTCCGGG TTCGGCAATA ACCTGGAGCC GCGCGCGTAG GTTGGCTCTT TAGGGCTTCA 60
CCCCGAAGCT CCACCTTCGC TCCCGTCTTT CTGAAACAC CGCTTTGATC TCGGCGGTGC 120
GGGACAGACG CTAGTGTGAG CCNMC ATG GCA GAT ACG ACC CCG AAC GGC CCC 172
 Met Ala Asp Thr Thr Pro Asn Gly Pro
 -50 -45
CAA GGG GCG GGC GCT GTG CAA TTC ATG ATG ACC AAT AAA CTG GAC ACG 220
Gln Gly Ala Gly Ala Val Gln Phe Met Met Thr Asn Lys Leu Asp Thr
 -40 -35 -30
GCA ATG TGG CTT TCT CGC TTG TTC ACA GTT TAC TGC TCT GCT CTG NNT 268
Ala Met Trp Leu Ser Arg Leu Phe Thr Val Tyr Cys Ser Ala Leu Xaa
 -25 -20 -15
GTT CTG CCT CTT CTT GGG TTG CAT GAA GCA GCA AGC TTT TAC CAA CGT 316
Val Leu Pro Leu Leu Gly Leu His Glu Ala Ala Ser Phe Tyr Gln Arg
 -10 -5 1 5
GCT TTG CTG GCA AAT GCT CTT ACC AGT GCT CTG AGG CTG CAT CAA AGA 364
Ala Leu Leu Ala Asn Ala Leu Thr Ser Ala Leu Arg Leu His Gln Arg
 10 15 20
TTA CCA CAC TTC CAG TTA AGC AGA GCA TTC CTG GCC CAG GCT TTG TTA 412
Leu Pro His Phe Gln Leu Ser Arg Ala Phe Leu Ala Gln Ala Leu Leu
 25 30 35
GAG GAC AGC TGC CAC TAC CTG TTG TAT TCA CTC ATC TTT GTA AAT TCC 460
Glu Asp Ser Cys His Tyr Leu Leu Tyr Ser Leu Ile Phe Val Asn Ser
 40 45 50
TAT CCA GTT ACA ATG AGT ATC TTC CCA GTC TTG TTA TTC 499
Tyr Pro Val Thr Met Ser Ile Phe Pro Val Leu Leu Phe
 55 60 65

```

## (2) INFORMATION FOR SEQ ID NO: 189:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 45..221

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93  
region 1..177  
id HUMHBC4659  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 63..221

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94  
region 1..159  
id AAL60569  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 124..159

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 97..132  
id R88362  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 1..72

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5  
seq XVLVLSVVXXAMA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG CGT TTC CGC CAT TTT TGM AAA TWA ATT GGG MAG GTA CTG GTT TTA | 48  |
| Met Arg Phe Arg His Phe Xaa Lys Xaa Ile Gly Xaa Val Leu Val Leu |     |
| -20 -15 -10                                                     |     |
| AGT GTA GTT SCC GMC GCA ATG GCA GCC TTT GCA GTG SHA CCT CAG GGG | 96  |
| Ser Val Val Xaa Xaa Ala Met Ala Ala Phe Ala Val Xaa Pro Gln Gly |     |
| -5 1 5                                                          |     |
| CCC GCG TTA SSM TCT GAA CCA MTG MTG CYG GGT TCA CCC ACA TCT CCA | 144 |
| Pro Ala Leu Xaa Ser Glu Pro Xaa Xaa Xaa Gly Ser Pro Thr Ser Pro |     |
| 10 15 20                                                        |     |
| AAG CCA GGA GTT AAT GCC CAG TTC TTA CCT GGA TTT TTA ATG GGG GMT | 192 |
| Lys Pro Gly Val Asn Ala Gln Phe Leu Pro Gly Phe Leu Met Gly Xaa |     |
| 25 30 35 40                                                     |     |

TTG CCA GCT CCG GTG ACT CCA CAA CCT  
Leu Pro Ala Pro Val Thr Pro Gln Pro  
45

219

## (2) INFORMATION FOR SEQ ID NO: 190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 105..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..310  
id T26956  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..359
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..315  
id T31666  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 202..332
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 137..267  
id R14990  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 127..201
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 63..137  
id R14990  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..114
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..50  
id R14990  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 1..120  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.2  
seq LCVEFASVASCDA/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG GAG TTG GGG AGT TGC CTG GAG GGC GGG AGG GAG GCG GCG GAG GAA | 48  |
| Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu |     |
| -40 -35 -30 -25                                                 |     |
| GAG GGC GAG CCT GAG GTG AAA AAG CGG CGA CTT CTG TGT GTG GAG TTT | 96  |
| Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Val Glu Phe |     |
| -20 -15 -10                                                     |     |
| GCC TCG GTC GCA AGC TGC GAT GCC GCA GTG GCT CAG TGC TTC CTG GCC | 144 |
| Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala |     |
| -5 1 5                                                          |     |
| GAG AAC GAC TGG GAG ATG GAA AGG GCT CTG AAC TCC TAC TTC GAG CCT | 192 |
| Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro |     |
| 10 15 20                                                        |     |
| CCG GTG GAG GAG AGC GCC TTG GAA CGC CGA CCT GAA ACC ATC TCT GAG | 240 |
| Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Glu Thr Ile Ser Glu |     |
| 25 30 35 40                                                     |     |
| CCC AAG ACC TAT GTT GAC CTA ACC AAT GAA GAA ACA ACT GAT TCC ACC | 288 |
| Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu Thr Thr Asp Ser Thr |     |
| 45 50 55                                                        |     |
| ACT TCT AAA ATC AGC CCA TCT GAA GAT ACT CAG CAA GAA AAT GGC AGC | 336 |
| Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln Gln Glu Asn Gly Ser |     |
| 60 65 70                                                        |     |
| ATG TTC TCT CTC ATT ACC TGG AAT ATT GAT GGA TTA GAT CTA AAC AAT | 384 |
| Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly Leu Asp Leu Asn Asn |     |
| 75 80 85                                                        |     |
| CTG TCA GAG AGG GCT CGA GGG GTG TGT TCC TAC TTA GCT TTG TAC AGC | 432 |
| Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr Leu Ala Leu Tyr Ser |     |
| 90 95 100                                                       |     |
| CCA GAT GTG ATA TTT CTA CAG GAA GTT ATT CCC CCA TAT TAT AGC TAC | 480 |
| Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro Pro Tyr Tyr Ser Tyr |     |
| 105 110 115 120                                                 |     |
| CTA                                                             | 483 |
| Leu                                                             |     |

## (2) INFORMATION FOR SEQ ID NO: 191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 182..401
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 165..384  
id W56608  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 30..115  
id W56608  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 127..191
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 111..175  
id W56608  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..446
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 385..430  
id W56608  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 311..446
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..136  
id R17248  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 13..378
- (C) IDENTIFICATION METHOD: Von Heijne matrix



(D) OTHER INFORMATION: score 5  
seq RLVVVSVSPQSRA/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

```

AGTGCGGCCG TC ATG GCG TCG CCC TTC AGC GGG GCG CTG CAG CTG ACG GAC 51
 Met Ala Ser Pro Phe Ser Gly Ala Leu Gln Leu Thr Asp
 -120 -115 -110

CTG GAT GAC TTC ATC GGG CCG TCT CAG GAG TGC ATC AAG CCT GTC AAA 99
Leu Asp Asp Phe Ile Gly Pro Ser Gln Glu Cys Ile Lys Pro Val Lys
 -105 -100 -95

GTG GAA AAA AGG GCG GGA AGT GGC GTG GCC AAG ATT CGC ATT GAA GAT 147
Val Glu Lys Arg Ala Gly Ser Gly Val Ala Lys Ile Arg Ile Glu Asp
 -90 -85 -80

GAC GGG AGC TAC TTC CAA ATT AAC CAA GAC GGC DGG ACC CGG AGG CTG 195
Asp Gly Ser Tyr Phe Gln Ile Asn Gln Asp Gly Xaa Thr Arg Arg Leu
 -75 -70 -65

GAG AAG GCC AAG GTC TCG CTA AAC TAC TGC NWG GCG TGC AGC GGC TGC 243
Glu Lys Ala Lys Val Ser Leu Asn Tyr Cys Xaa Ala Cys Ser Gly Cys
 -60 -55 -50

ATC ACC TCC GCA GAG ACC GTG CTT ATC ACC CAG CAG AGC CAC GAG GAG 291
Ile Thr Ser Ala Glu Thr Val Leu Ile Thr Gln Gln Ser His Glu Glu
 -45 -40 -35 -30

CTG AAG AAG GTT CTA GAT GCT AAC AAG ATG GCG GCA CCC AGT CAG CAG 339
Leu Lys Lys Val Leu Asp Ala Asn Lys Met Ala Ala Pro Ser Gln Gln
 -25 -20 -15

AGG CTG GTT GTA GTT TCG GTC TCA CCA CAG TCT AGA GCA TCG CTG GCT 387
Arg Leu Val Val Val Ser Val Ser Pro Gln Ser Arg Ala Ser Leu Ala
 -10 -5 1

GCA CGG TTT CAG CTG AAW CCT ACA GAT ACT GCC AGG AAA TTA ACC TCA 435
Ala Arg Phe Gln Leu Xaa Pro Thr Asp Thr Ala Arg Lys Leu Thr Ser
 5 10 15

TTC TTT AAA
Phe Phe Lys
20

```

(2) INFORMATION FOR SEQ ID NO: 192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 base pairs
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: DOUBLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..97
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 1..54  
id H30111  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 84..215
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq SLVAELLLGAGSG/SH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

```

ATACTTTCTG YAGYAGTCCT GGACCTCCTG TGCAAGAACA TGAAACACCT GTGGTTCATC 60
CTCCTGCTGG TGGCAGCTCC CAG ATG GGT CCT GTC CCG ACT GCA GTT GCA GGG 113
 Met Gly Pro Val Pro Thr Ala Val Ala Gly
 -40 -35

GCT GGC TCA CGA CTG GTA AAG CCC TCA CAG ACC CTG TCC CTC ACC TGC 161
Ala Gly Ser Arg Leu Val Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys
 -30 -25 -20

GCT GTC TCT GGT GGC TCA TTA GTA GCG GAA CTT CTT CTT GGA GCT GGA 209
Ala Val Ser Gly Gly Ser Leu Val Ala Glu Leu Leu Leu Gly Ala Gly
 -15 -10 -5

TCC GGC AGT CAC CTG GGA CGG GCC TGG AGT GGA TTG GGT TCA TCT ATT 257
Ser Gly Ser His Leu Gly Arg Ala Trp Ser Gly Leu Gly Ser Ser Ile
 1 5 10

ATA GAG GCA ATA GTG GGA GTA CTT CTT ACA ATC CGT CCC TCA AGA CTC 305
Ile Glu Ala Ile Val Gly Val Leu Leu Thr Ile Arg Pro Ser Arg Leu
 15 20 25 30

GAG CCA CCA TAT CAC TGG ACA AGC CCC GCG 335
Glu Pro Pro Tyr His Trp Thr Ser Pro Ala
 35 40

```

## (2) INFORMATION FOR SEQ ID NO: 193:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 222..359  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
 region 33..170  
 id T50032  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 348..393  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 160..205  
 id T50032  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 189..229  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 1..41  
 id T50032  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 128..196  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.4  
 seq QFILLGTTSVVTA/AL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

```

GACTGATTTC GAGTTTCCGG TCAGGTTAGG CCGGGGGGGT GCGGTCCTGG TCGGAAGGAG 60
GTGGAGAGTC GGGGGTCACC AGGCCTATCC TTGGCGCCAC AGTCGGCCAC CGGGGCTCGC 120
CGCCGTC ATG GAG AGC GGA GGG CGG CCC TCG CTG TGC CAG TTC ATC CTC 169
Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu
 -20 -15 -10

CTG GGC ACC ACC TCT GTG GTC ACC GCC GCC CTG TAC TCC GTG TAC CGG 217
Leu Gly Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg
 -5 1 5

CAG AAG GCC CGG GTC TCC CAA GAG CTC AAG GGA GCT AAA AAA GTT CAT 265
Gln Lys Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His
 10 15 20

TTG GGT GAA GAT TTA AAG AGT ATT CTT TCA GAA GST CCA GGA AAA TGC 313
Leu Gly Glu Asp Leu Lys Ser Ile Leu Ser Glu Xaa Pro Gly Lys Cys
 25 30 35

GTG CCT TAT GCT GTT ATA GAA GGA GCT GTG CGG TCT GTT AAA GAA ACG 361
Val Pro Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr
 40 45 50 55

```

CTT AAC ACC CAG TTT GTG GAA AAC TGC AAG  
Leu Asn Ser Gln Phe Val Glu Asn Cys Lys  
60 65

391

## (2) INFORMATION FOR SEQ ID NO: 194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 269..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 2..75  
id R33746  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 391..459
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 124..192  
id R33746  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 344..391
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 78..125  
id R33746  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 397..453
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq IYIICFXLPPLFS/FN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

ATATATAAAT GTTTCATGTT ATTGGTTTGG TACCTAGTCC TTTGCATGGA TATATAGGTA 60  
CCTAATGAAA ATCGAGGATC AGTGTATGAC AAATCTCCCA TCCTCCCCTT TCCTTATTGC 120

```

CTGTCTCCGC AATAGGAAGT AGAATAGTTG TGTGTTSTTT ACTTACTTST CTGTTTITAGA 180
GAGAITTTCTA TTTTGGTAG GGAATATTC TAATATGTTT TCATATCTTT ATTTCATTTT 240
GTAGTCTTTT GCATGGCTAT GTAGGGACCT AATGAAAGTC GASTTTCATA ATATSACAGC 300
TCACDTCTTT TCCTACATAT TTCCTCACTT AGCAGTAGCT WGNKAGTTAT KTTSTGGTTA 360
TTTTATTICA TTCTCTAGGA TCTATTCCAT TIGNNG ATG CAA GTG TWT AGA TGC 414
 Met Gln Val Cys Arg Cys
 -15

ATA TAT ATC ATT TGC TTC TWT CTT CCG CCA TTA TTT TCC TTT AAC 459
Ile Tyr Ile Ile Cys Phe Xaa Leu Pro Pro Leu Phe Ser Phe Asn
 -10 -5 1

```

## (2) INFORMATION FOR SEQ ID NO: 195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..193
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 96.1  
region 1..152  
id HSU78678  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 90..171  
id N41898  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 95..176  
id H69272  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 112..193  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 39..120  
id N20619  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 44..88  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.1  
seq QRLLLRFLASVIS/RK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GGGAGGGCTA GGCTGTGCAT CCCTCCGCTC GCATTGCAGG GAG ATG GCT CAG CGA | 55  |
| Met Ala Gln Arg                                                 |     |
| -15                                                             |     |
| CTT CTT CTG AGG TTC CTG GCC TCT GTC ATC TCC AGG AAG CCC TCT CAR | 103 |
| Leu Leu Leu Arg Phe Leu Ala Ser Val Ile Ser Arg Lys Pro Ser Gln |     |
| -10 -5 1 5                                                      |     |
| GGT CAG TGG GCC ACC CCT CAC TTC CAG AGC CCT GCA GAC CCC ACA ATG | 151 |
| Gly Gln Trp Ala Thr Pro His Phe Gln Ser Pro Ala Asp Pro Thr Met |     |
| 10 15 20                                                        |     |
| CAG TCC TGG TGG CCT GAC TGT AAC ACC CAA CCC AGC CCG GAC         | 193 |
| Gln Ser Trp Trp Pro Asp Cys Asn Thr Gln Pro Ser Pro Asp         |     |
| 25 30 35                                                        |     |

## (2) INFORMATION FOR SEQ ID NO: 196:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 111..277  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 3..169  
id AA149704  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 143..262  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
 seq FLWLITRPPQPVLP/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

```

AAGTCCTAGG AGCTGTGGAA AGAGTAGAAG TGCCTGAATG TGGTGCTGAA TCAATACAGC 60
CAGCTGTGAG GGGAGCACTT CCTGGACCCA GGAAGGGAGA GTCTTCTTCC AAGGTCTGAA 120
TTTCTGCTG CTGTTACAAA AG ATG CTT TTT ATC TTT AAC TTT TTG TTT TCC 172
 Met Leu Phe Ile Phe Asn Phe Leu Phe Ser
 -40 -35

CCA CTT CCG ACC CCG GCG TTG ATC TGC ATC CTG ACA TTT GGA GCT GCC 220
Pro Leu Pro Thr Pro Ala Leu Ile Cys Ile Leu Thr Phe Gly Ala Ala
-30 -25 -20 -15

ATC TTC TTG TGG CTG ATC ACC AGA CCT CAA CCC GTC TTA CCT CTT CTT 268
Ile Phe Leu Trp Leu Ile Thr Arg Pro Gln Pro Val Leu Pro Leu Leu
 -10 -5 1

GAC CTG AAC CKG 280
Asp Leu Asn Xaa
5

```

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 323..443
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 2..122  
id R84934  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 323..390
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..68  
id AA020970  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 373..443  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 52..122  
                           id AA020870  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(407..438)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
                           region 42..73  
                           id AA187611  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 297..434  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
                           seq SHMLQLLPKALC/LF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

```

TTTGTGGGCT CCTCTTTGGG GTGACCACTG CTTTCAAAGC CATCTGCCAA GGCTCTCCAG 60
GGCAGGACCT GACTGGTGGG GAATGAGTGT TCAGAAGCCT TGGGAGAGGC CAAAGAGCCA 120
TTCTAGGATG RTCKGAGGAA AACCTTCCTG CAGAGGCCAG AAACCTTGAG CTTAGGTGCC 180
TGGGGACCAG CTTCGACATT CTCTCCAGTT TCTGATTCTA ATTTTGGCCA CGTGTCACAA 240
CTTTTCCAGT CTCTGAGAAG GTCCCAGVCT TTCTCAAATA TTCTGATTTT GAAAAT ATG 299
 Met
TAT CCA AAG TGG GAG GCC CCT GTG ACA TTT TGC CAA CTT AAA CGA GAA 347
Tyr Pro Lys Trp Glu Ala Pro Val Thr Phe Cys Gln Leu Lys Arg Glu
-45 -40 -35 -30
AAA GAC CCC CCG CAC CCG GCA CAC TCC CCC TTC CTC CAG CCC CGC TTC 395
Lys Asp Pro Pro His Pro Ala His Ser Pro Phe Leu Gln Pro Arg Phe
-25 -20 -15
AGC CAC ATG CTC CAG CTG CTG CCC AGT AAA GCC CTG TGC CTT TTT TTC 443
Ser His Met Leu Gln Leu Leu Pro Ser Lys Ala Leu Cys Leu Phe Phe
-10 -5 1

```

## (2) INFORMATION FOR SEQ ID NO: 198:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 42..151

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: Identity 98  
region 1..110  
id AA121585  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 143..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: Identity 95  
region 101..172  
id AA121585  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 42..136

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 1..95  
id AA100539  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 143..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95  
region 100..171  
id AA100539  
est

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: 36..167

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.7  
seq LAERLGLFEELWA/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

ACTGTTTGAG GATGTAGGCA CTGGTGTGAA GGAAC ATG GCC CTG TAT CAG AGG 53  
Met Ala Leu Tyr Gln Arg  
-40

TGG CGG TGT CTC CGG CTC CAA GGT TTA CAG GCT TGC AGG CTA CAC ACG 101  
Trp Arg Cys Leu Arg Leu Gln Gly Leu Gln Ala Cys Arg Leu His Thr  
-35 -30 -25

```

GCA GTT GTG TCG ACC COT CCA CGC TGG TTG GCA GAG CGG CTT GGC CTT 149
Ala Val Val Ser Thr Pro Pro Arg Trp Leu Ala Glu Arg Leu Gly Leu
 -20 -15 -10

TTT GAG GAG CTG TGG GCT GCT CAG GTA AAG AGA TTA GCA AGC ATG GCA 197
Phe Glu Glu Leu Trp Ala Ala Gln Val Lys Arg Leu Ala Ser Met Ala
 -5 1 5 10

CAG AAG GAA CCC CAG ACG 215
Gln Lys Glu Pro Gln Thr
 15

```

## (2) INFORMATION FOR SEQ ID NO: 199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 57..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 22..241  
id C16912  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 172..260
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 64..152  
id T68684  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..164
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 26..58  
id T68684  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig peptide
- (B) LOCATION: 93..166
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.8  
seq XGLLLFLLPGSLG/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

```

AGAGAGAGGA ACTGGGGTCT CCAGTCACGG GAGCCAGGAG CCGGCCAGGG CCCGAGSAGG 60
AAGGGAGCGA GGCTGAAGGG AACGTCGTCC TCTCAGC ATG GGG GTC CCG CGG CCT 115
 Met Gly Val Pro Arg Pro
 -20

CAG CCC TGG GCG STG GGG CTC CTG CTC TTT CTC CTT CCT GGG AGC CTG 163
Gln Pro Trp Ala Xaa Gly Leu Leu Leu Phe Leu Leu Pro Gly Ser Leu
 -15 -10 -5

GGC GCA GAA AGC CAC CTC TCC CTC CTG TAC CAC CTT ACC GCG GTG TCC 211
Gly Ala Glu Ser His Leu Ser Leu Leu Tyr His Leu Thr Ala Val Ser
 1 5 10 15

TCG CCT GCC CCG GGG ACT CCT GCC TTC TGG GTG TCC GGC TGG CTG GGC 259
Ser Pro Ala Pro Gly Thr Pro Ala Phe Trp Val Ser Gly Trp Leu Gly
 20 25 30

CCG CAG CAG TAC CCG AGC CAG 280
Pro Gln Gln Tyr Pro Ser Xaa
 35

```

## (2) INFORMATION FOR SEQ ID NO: 200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..249
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 5..252  
id C18087  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 166..350
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 20..204  
id AA018305  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 187..350  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 42..205  
id AA015592  
est

(1x) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 181..350  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 33..202  
id AA018631  
est

(ix) FEATURE:

[illegible]

(ix) FEATURE:

[illegible]

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 28..162  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 13.4  
seq LVLALXDVSAALS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

|            |            |         |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|------------|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AAGCGCAGGC | TCCCAGCCGA | GTCCGTT | ATG | GCC | GCT | GCC | CTC | CCG | AAG | AGG | ATG | 54  |     |     |     |     |
|            |            |         | Met | Ala | Ala | Ala | Val | Pro | Lys | Arg | Met |     |     |     |     |     |
|            |            |         | -45 |     |     |     |     |     | -40 |     |     |     |     |     |     |     |
| AGG        | GGG        | CCA     | GCA | CAA | GCG | AAA | CTG | CTG | CCC | GGG | TCG | GCC | ATC | CAA | GCC | 102 |
| Arg        | Gly        | Pro     | Ala | Gln | Ala | Lys | Leu | Leu | Pro | Gly | Ser | Ala | Ile | Gln | Ala |     |
|            | -35        |         |     |     |     | -30 |     |     |     |     | -25 |     |     |     |     |     |
| CTT        | GTG        | GGG     | TTG | GCG | CGG | CCG | CTG | GTC | TTG | GCG | CTC | VTG | CTT | GTG | TCC | 150 |
| Leu        | Val        | Gly     | Leu | Ala | Arg | Pro | Leu | Val | Leu | Ala | Leu | Xaa | Leu | Val | Ser |     |
|            | -20        |         |     |     | -15 |     |     |     |     | -10 |     |     |     |     | -5  |     |
| GCC        | GCT        | CTA     | TCC | AGT | GTT | GTA | TCA | CGG | ACT | GAT | TCA | CCG | AGC | CCA | ACC | 198 |
| Ala        | Ala        | Leu     | Ser | Ser | Val | Val | Ser | Arg | Thr | Asp | Ser | Pro | Ser | Pro | Thr |     |
|            |            |         |     | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GTA CTC AAC TCA CAT ATT TCT ACC CCA AAT GTS AAT GGT TTA ACA CAT | 246 |
| Val Leu Asn Ser His Ile Ser Thr Pro Asn Val Asn Ala Leu Thr His |     |
| 15 20 25                                                        |     |
| GAA AAC CAA ACC AAA CCT TCT ATT TCC CAA ATC ACC ACC ACC CTC CCT | 294 |
| Glu Asn Gln Thr Lys Pro Ser Ile Ser Gln Ile Ser Thr Thr Leu Pro |     |
| 30 35 40                                                        |     |
| CCC AYT NCG AGT ACC AAG VNA AGT GGA GGA GCA TYT GTS GTC CCT CAT | 342 |
| Pro Xaa Xaa Ser Thr Lys Xaa Ser Gly Gly Ala Xaa Val Val Pro His |     |
| 45 50 55 60                                                     |     |
| CCC TCG CCA GGG                                                 | 354 |
| Pro Ser Pro Gly                                                 |     |

## (2) INFORMATION FOR SEQ ID NO: 201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 170..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 117..269  
id HSC3DG011  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..184
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 1..132  
id HSC3DG011  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(177..209)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 337..369  
id H41589  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 137..223

(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 13  
 seq LLLVLLLVTRXRS/MP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

```

AATTTGTGGC SCGCTGGTCC CCTCAGAGGG TTCCTGCTGC TCCCGGTGCC TTGGACCCTC 60
CCCCCTCGCTT CSNGTTCTAC TGCCCCAGGA GCCCCGCGGG TCCGGGACTC CCGKCCGTGC 120
CGGTGCGGGC GCCGGC ATG TGG CTG TGG GAG GAC CAG GGC GGC CTC CTG GGC 172
 Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly
 -25 -20

CCT TTC TCC TTC CTG CTG CTA GTG CTG CTG CTG GTG ACG CGG ASC CGG 220
Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Xaa Arg
 -15 -10 -5

TCA ATG CCT GCC TCC TCA CCG GCA GCC TCT TCG TTC TAC TGC GCG TCT 268
Ser Met Pro Ala Ser Ser Pro Ala Ala Ser Ser Phe Tyr Cys Ala Ser
 1 5 10 15

TCA GCT BTG AGC CGG TGC CCT CTT GCA GGG CCC TGC ACG TGC TCA AGC 316
Ser Ala Xaa Ser Arg Cys Pro Leu Ala Gly Pro Cys Arg Cys Ser Ser
 20 25 30

CCC GGG ACC GCA TTT CTG 334
Pro Gly Thr Ala Phe Leu
 35

```

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..280
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 28..284  
id R02745  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..176
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 6..179  
id T84331  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 172..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 176..284  
id T84331  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 27..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..254  
id AA017512  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 27..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..254  
id N95074  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 173..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 146..253  
id N75564  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 65..151  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 40..126  
id N75564  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 27..66  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 1..40  
id N75564  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 36..119

(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 11.6  
 seq LLLLVQLLRFLRA/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

```

ATTTCCTCCC CCCGAGCTGG GCGTGGCGGG CCGCA ATG AAC TGG GAG CTG CTG 53
 Met Asn Trp Glu Leu Leu
 -25

CTG TGG CTG CTG GTG CTG TGC GCG CTG CTC CTG CTC TTG GTG CAG CTG 101
Leu Trp Leu Leu Val Leu Cys Ala Leu Leu Leu Leu Leu Val Gln Leu
-20 -15 -10

CTG CGC TTC CTG AGG GCT GAC GGC GAC CTG ACG CTA CTA TGG GCC GAG 149
Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu Thr Leu Leu Trp Ala Glu
-5 1 5 10

TGG CAG GGA CGA CGC CCA GAA TGG GAG CTG ACT GAT ATG GTG GTG TGG 197
Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu Thr Asp Met Val Val Trp
 15 20 25

GTG ACT GGA GCC TCG AGT GGA ATT GGT GAG GAG CTG GCT TAC CAG TTG 245
Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu Leu Ala Tyr Gln Leu
 30 35 40

TCT AAA CTA GGA GTT TGT CTT GTG CTG TCA GCC AGG 281
Ser Lys Leu Gly Val Ser Leu Val Leu Ser Ala Arg
 45 50

```

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 163..344
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 35..216  
id T86663  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 163..278
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97



region 43..158  
id AA055850  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 177..236  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 11.2  
seq AFLLLVALSYTLA/RD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

AGAAGATAAT CACTTGGGGA AAGGAAGGTT CGTTTCTGAG TTAGCAACAA GTAAATGCAG 60  
CACTAGTGGG TGGGATTGAG GTATGCCCTG GTGCATAAAT AGAGACTCAG CTGTGCTGGC 120  
ACACTCAGAA GCTTGGACCG CATCCTAGCC GCCGACTCAC ACAAGGCAGA GTTGCC ATG 179  
Met  
-20  
GAA AAA ATT CCA GTG TCA GCA TTC TTG CTC CTT GTG GCC CTC TCC TAC 227  
Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Val Ala Leu Ser Tyr  
-15 -10 -5  
ACT CTG GCC AGA GAT ACC ACA GTC AAA CCT GGA GCC AAA AAG GAC ACA 275  
Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp Thr  
1 5 10  
AAG GAC TCT CGA CCC AAA CTG CCC CAG ACC CTC TCC AGA GGT TGG GGT 323  
Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp Gly  
15 20 25  
GAC CAA CTC ATC TGG ACA CGG 344  
Asp Gln Leu Ile Trp Thr Arg  
30 35

## (2) INFORMATION FOR SEQ ID NO: 204:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 171..312  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 33..174  
id T86663

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 171..288
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 41..158  
id AA055880  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 127..246
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2  
seq AFLLLVALSYTLA/RD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

```
AAGATTCACA AGGCCAACAG ACAACCCAAA GTCATTAAGC CATGAGAGTG GAATGAATCT 60
ATGAAAACTC AATGAAGACA GAACAAGAGA AAAATCTTTT CAGCCACGAT GAATTAGGRG 120
ACAAG ATG TCA AAT TAC ACT GAT GCT GAG TCA AGC TTC TCA AAG CAA 168
 Met Ser Asn Tyr Thr Asp Ala Glu Ser Ser Phe Ser Lys Gln
 -40 -35 -30
GAG ATA ATC AGA GTT GCC ATG GAG AAA ATT CCA GTG TCA GCA TTC TTG 216
Glu Ile Ile Arg Val Ala Met Glu Lys Ile Pro Val Ser Ala Phe Leu
 -25 -20 -15
CTC CTT GTG GCC CTC TCC TAC ACT CTG GCC AGA GAT ACC ACA GTC AAA 264
Leu Leu Val Ala Leu Ser Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys
 -10 -5 1 5
CCT GGA GCC AAA AAG GAC ACA AAG GAC TCT CGA CCC AAA CCG CCC CGG 312
Pro Gly Ala Lys Lys Asp Thr Lys Asp Ser Arg Pro Lys Pro Pro Arg
 10 15 20
```

## (2) INFORMATION FOR SEQ ID NO: 205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 96..165
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 364..433  
id AA100852  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 45..95  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 314..364  
id AA100852  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 14..46  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 282..314  
id AA100852  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 96..202  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 65..171  
id AA113841  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 31..95  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..65  
id AA113841  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 290..324  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 326..360  
id AA133048  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 158..191  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 2..35  
id AA133048  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 169..290  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 1..122  
                           id AA159272  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 53..95  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 323..365  
                           id AA161042  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 96..138  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 365..407  
                           id AA161042  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 14..46  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 282..314  
                           id AA161042  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 3..161  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 10.6  
                           seq FILLLLIFIAEVAA/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AC ATG CAG TTT GNA ACG TGG GCT ACT TCC TCA TCG CAG CCG GCG TTG  | 47  |
| Met Gln Phe Xaa Thr Trp Ala Thr Ser Ser Ser Gln Pro Ala Leu     |     |
| -50 -45 -40                                                     |     |
| TGG TCT TTG CTC TTG GTT TCC TGG GCT GCT ATG GTG CTA AGA CTG AGA | 95  |
| Trp Ser Leu Leu Leu Val Ser Trp Ala Ala Met Val Leu Arg Leu Arg |     |
| -35 -30 -25                                                     |     |
| AGC AAG TGT GCC CTC GTG ACG TTC TTC TTC ATC CTC CTC ATC TTC     | 143 |
| Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile Phe |     |
| -20 -15 -10                                                     |     |
| ATT GGT GAG GTT GCA GCT GCT GTG GTC GCC TTG GTG TAC AAC ACA ATG | 191 |
| Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Xaa Thr Met |     |
| -5 1 5 10                                                       |     |
| BCT GAG CAC TTC CTG ACG TTG CTC GTA GTG GCT GCC ATC AAG AAA GAT | 239 |

```

Xaa Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys Asp
 15 20 25

TAT GGT TCC CAG GAA GAC TTC ACT CAA GTG TGG AAC ACC ACC ATG AAA 287
Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Xaa Asn Thr Thr Met Lys
 30 35 40

GGG CTC AAG TGC TGT GGC TTC ACC AAC TAT ACG GAC TGG 326
Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Trp
 45 50 55

```

## (2) INFORMATION FOR SEQ ID NO: 206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 147..283  
id N36076  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..140
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 40..148  
id N36076  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 287..333
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 296..342  
id N36076  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..33
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 8..40  
id N36076

est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..333  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 9..340  
id N95074  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..333  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 9..340  
id AA017512  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 140..333  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 146..339  
id W04626  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 5..140  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 12..147  
id W04626  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 45..334  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 47..336  
id H27747  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 1..34  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..34  
id H27747  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 3..36  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 10.5

seq LLLLVHLLRFLRA/DG

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

```

AA ATG AAC TGG GAG CTG CTG CTG TGG CTG CTG GTG CTG TGC GCG CTG 47
Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu
 -25 -20 -15

CTC CTG CTC TTG GTG CAT CTG CTG CGC TTC CTG AGG GCT GAC CGC GAC 95
Leu Leu Leu Leu Val His Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp
 -10 -5 1

CTG ACC CTA CTA TGG GCC GAG TGG CAG GGA CGA CGC CCA GAA TGG GAG 143
Leu Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu
 5 10 15

CTG ACT GAT ATG GTG GTG TGG GTG ACT GGA GCC TCG AGT GGA ATT GGT 191
Leu Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly
 20 25 30 35

GAG GAG CTG GGT TAC CAG TTG TCT AAA CTA GGW KTT TCT CTT GTG CTG 239
Glu Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Xaa Ser Leu Val Leu
 40 45 50

TCA GCC AGA AGA GTG CAT GAG CTG GAA AGG GTG AAA AGA AGA TGC CTA 287
Ser Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu
 55 60 65

GAG AAT GGC AAT TTA ARA GAA AAA GAT ATA CTT GTT TTG CCC CTT GGG 335
Glu Asn Gly Asn Leu Xaa Glu Lys Asp Ile Leu Val Leu Pro Leu Gly
 70 75 80

```

(2) INFORMATION FOR SEQ ID NO: 207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..162
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 424..533  
id N80896  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(283..318)

(C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 342..377  
 id W16973  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 293..347  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 1..55  
 id R02710  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 120..272  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 10.3  
 seq VSCLTLWSPGCWP/QP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

```

TGCACIATGC TTGTGTGTAT GTGTGTGCCT CTGTCTTGCT CTCTTATCTC CCAGCAGTGA 60
GACATTGGAC GTSTTTGCTC ATGAAGATGC AGTATATGGC TTGTCTGTGA GCCCASTGA 119
ATG ACA ACA TTT TTG CCA GTT CCT CAG ATG ATG GCC GGG TTC TCA TTT 167
Met Thr Thr Phe Leu Pro Val Pro Gln Met Met Ala Gly Phe Ser Phe
-50 -45 -40

GGG ACA TTC GSG AAT CCC CCC ATG GAG AGC CCT TCT GCC TGG CAA ACT 215
Gly Thr Phe Gly Asn Pro Pro Met Glu Ser Pro Ser Ala Trp Gln Thr
-35 -30 -25 -20

ATC CAT CAG CCT TTC ATA GTG TCA TGT TTA ACC CTG TGG ACC CCA GGT 263
Ile His Gln Pro Phe Ile Val Ser Cys Leu Thr Leu Trp Ser Pro Gly
-15 -10 -5

TGT TGG CCA CAG CCA ATT CAA AGG AAG GAG TGG GAC TCT GGG ACA TTC 311
Cys Trp Pro Gln Pro Ile Gln Arg Lys Glu Trp Asp Ser Gly Thr Phe
1 5 10

GAA AAC CTC AGA GTT CTC TCC TGC GCT ATG GTG GAA 347
Glu Asn Leu Arg Val Leu Ser Cys Ala Met Val Glu
15 20 25

```

## (2) INFORMATION FOR SEQ ID NO: 208:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA



## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 168..461  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 47..340  
id N39924  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 169..370  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 178..379  
id R61601  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 359..431  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 369..441  
id R61601  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 75..158  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.5  
seq LVXFSL LATAILG/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```

ACCATAGCAA ATTAAATGAC TGCCATAAAG TATATTTTAC TCACAGGACA GATTACAATA 60
GCCTTGATAG AATC ATG GCA TCC AAA GGG ATG CGC CAT TTT TCC TTG ATT 110
 Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile
 -25 -20

TCA GAG CAG TTG GTG TYC TTT AGT CTT CTT GCA ACA GCG ATT TTG GGA 158
Ser Glu Gln Leu Val Xaa Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly
-15 -10 -5

GCA GTT TCC TGG CAG CCA ACA AAT GGA ATT TTC TTG AGC ATG TTT CTA 206
Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu
 1 5 10 15

ATC GTT TTG CCA TTG GAA TCC ATG GCT CAT GGG CTC TTC CAT GAA TTG 254
Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu
 20 25 30

GGT AAC TGT TTA GGA GGA ACA TCT GTT GGA TAT GCT ATT GTG ATT CCC 302
Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro

```

| 35                                                              | 40 | 45 |     |
|-----------------------------------------------------------------|----|----|-----|
| ACC AAC TTC TGC AGT CCT GAT GGT CAG CCA ACA CTG CTT CCC CCA GAA |    |    | 350 |
| Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu |    |    |     |
| 50                                                              | 55 | 60 |     |
| CAT GTA CAG GAG TTA AAT TTG AGG TCT ACT GGC ATG CTC AAT GCT ATC |    |    | 398 |
| His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile |    |    |     |
| 65                                                              | 70 | 75 | 80  |
| CAA AGA TTT TTT GCA TAT CAT ATG ATT GAG ACC TAT GGA TGT GAC TAT |    |    | 446 |
| Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr |    |    |     |
| 85                                                              | 90 | 95 |     |
| TCC ACA AGT GGA CTG                                             |    |    | 461 |
| Ser Thr Ser Ser Gly Leu                                         |    |    |     |
| 100                                                             |    |    |     |

## (2) INFORMATION FOR SEQ ID NO: 209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(31..239)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 3..211  
id N27605  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..111)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..110  
id N78549  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 78..140
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3  
seq VLPVILLLLGAHP/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

```

AAGAGCAGAG CCGGAAGAAG GCGGGACGAA CCGGAAGAGG GTGAAATGCT TTCGGTAGGC 60
ACTCCACGGC TGTGAAG ATG GCG GCG GCT GCG TGG CTT CAG GTG TTG CCT 110
 Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro
 -20 -15

GTC ATT CTT CTG CTT CTG GGA GCT CAC CCG TCA GGA CTG TCG TTT TTC 158
Val Ile Leu Leu Leu Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe
-10 -5 1 5

AST GCG GGA CCG GCA ACC GTA GCT GCT GCC GAC CGG TCC AAA TGG CAC 206
Ser Ala Gly Pro Ala Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His
 10 15 20

RKT CCG ATA CCG TCG GGG AAA AAT TAT TTT AGT TTT GGA AAG ATC CTC 254
Xaa Pro Ile Pro Ser Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu
 25 30 35

TTC AGA AAT ACC ACT ATC TTC CTG AAG TTT GAT GGA GAA CGA 296
Phe Arg Asn Thr Thr Ile Phe Leu Lys Phe Asp Gly Glu Arg
 40 45 50

```

## (2) INFORMATION FOR SEQ ID NO: 210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..281
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 78..241  
id R57572  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..91
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..54  
id R57572  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..122
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93  
region 52..84  
id R57572  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 117..272  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 59..214  
id W55468  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 273..328  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 214..269  
id W55468  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 130..456  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.1  
seq LVLAVLFFHQLVG/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

```

ACTTTGTCAT TCAGCTGCCT GCTGCCTCCG CAGCGTCCCC CCAGCTCTCC CTGTGCTAAC 60
TGCCTGCACC TTGGACAGAG CGGGTGGCGA AATCAGAAGG ATTAGTTGGG ACCTGCCCTT 120
GGCGACCCC ATG GCA TCC CCC AGA ACC GTA ACT ATT GTG GCC CTC TCA GTG 171
Met Ala Ser Pro Arg Thr Val Thr Ile Val Ala Leu Ser Val
 -105 -100

GCC CTG GGA CTC TTC TTT GTT TTC ATG GGG ACT ATC AAG CTG ACC CCC 219
Ala Leu Gly Leu Phe Phe Val Phe Met Gly Thr Ile Lys Leu Thr Pro
-95 -90 -85 -80

AGG CTC ASC AAG GAT GCC TAC AGT GAG ATG AAA CGT GCN NAC AAG AGC 267
Arg Leu Ser Lys Asp Ala Tyr Ser Glu Met Lys Arg Ala Xaa Lys Ser
 -75 -70 -65

TAT GTT CGA GCC CTC CCT CTG CTG AAG AAA ATG GGG ATC AAT TCC ATT 315
Tyr Val Arg Ala Leu Pro Leu Leu Lys Lys Met Gly Ile Asn Ser Ile
 -60 -55 -50

CTC CTC CGA AAA AGC ATT GGT CCC CTT GAA GTG GCC TGT GGC ATC GTC 363
Leu Leu Arg Lys Ser Ile Gly Ala Leu Glu Val Ala Cys Gly Ile Val
 -45 -40 -35

ATG ACC CTT GTG CCT GGG CGT CCC AAA GAT GTG GCC AAC TTC TTC CTA 411
Met Thr Leu Val Pro Gly Arg Pro Lys Asp Val Ala Asn Phe Phe Leu
 -30 -25 -20

```

CTG TTG CTG GTG TTG GCT GTG CTC TTC TTC CAG CAG CTG GTC GST GAT 459  
Leu Leu Leu Val Leu Ala Val Leu Phe Phe His Gln Leu Val Gly Asp  
-15 -10 -5 1  
CCT CTC AAA 468  
Pro Leu Lys

## (2) INFORMATION FOR SEQ ID NO: 211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 84..217  
id AA021055  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..70  
id AA021055  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 84..217  
id W98068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..70  
id W98068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 38..191  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 11..114  
id AA059040  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 91..204  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.8  
seq LLLLCALHSHIYC/IK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

```
CATAAAATTT GAGGATATCA GCTGATTATT TTTTCTTCCM ASAATGAAAA TCAAGCAGAA 60
TTGATTCCTA CACGAAAAAA AAGCACACGA ATG CCA AAC CTT TCC TTT GGT GGA 114
 Met Pro Asn Leu Ser Phe Gly Gly
 -35

CTG GAC ACT AAC CAG ATG AGA GTA AAT TTC TTA TCC GTG GAC GTA TGT 162
Leu Asp Thr Asn Gln Met Arg Val Asn Phe Leu Ser Val Asp Val Cys
-30 -25 -20 -15

AAG CTA CTG CTG CTG TGT GCT CTC CAC AGC CAT ATT TAT TGT ATT AAA 210
Lys Leu Leu Leu Leu Cys Ala Leu His Ser His Ile Tyr Cys Ile Lys
 -10 -5 1

CAA TCA GCA CTT CGG 225
Gln Ser Ala Leu Arg
5
```

## (2) INFORMATION FOR SEQ ID NO: 212:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 134..373  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 115..359  
id R67703  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 23..135  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 5..117  
id R67703  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 134..318  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 115..299  
id H42383  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 20..135  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 2..117  
id H42383  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 193..383  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 87..277  
id W90193  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 134..192  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 29..87  
id W90193  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 417..454  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 314..351  
id W90193  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 288..470  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..183  
id R53752  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 258..422
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq XXLLLLNVGQLLA/QT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

```

AACCCACGGT GGGGGGAGCG CGGCCATGGC GTCCTGCTT TCGGTGCTGC GTGTACTGCT 60
GGGCGGCTTC TTCGCGCTCG TGGGGTTGGC CAAGCTCTCG GAGGAGATCT CGGCTCCAGT 120
TTGGGAGCGG RTGRAATGCC CTGTTCGTGC AGTTTGCTGA TGTGTTCCCG CTGAAGGTAT 180
TTGGCTACCA GCCAGATCCC CTGAACTACC AAATAGCTGT GGGCTTTCTG GAACTGCTGG 240
CTGGGTTGCT GCTGGTC ATG GGC CCA CCG ATG CTG CAA GAG ATC AGT AAC 290
 Met Gly Pro Pro Met Leu Gln Glu Ile Ser Asn
 -55 -50 -45

TTG TTC TTG ATT CTG CTC ATG ATG GGG GCT ATC TTC ACC TTG GCA GCT 338
Leu Phe Leu Ile Leu Leu Met Met Gly Ala Ile Phe Thr Leu Ala Ala
 -40 -35 -30

CTG AAA GAG TCA CTA AGC ACC TGT ATC CCA GCC ATT GTC TGC CTG NGG 386
Leu Lys Glu Ser Leu Ser Thr Cys Ile Pro Ala Ile Val Cys Leu Xaa
 -25 -20 -15

TDN CTG CTG CTG CTG AAT GTC GGC CAG CTC TTA GCC CAG ACT AAG AAG 434
Xaa Leu Leu Leu Leu Asn Val Gly Gln Leu Leu Ala Gln Thr Lys Lys
 -10 -5 1

GTG GTC AGA CCC ACT AGG AAG AAG ACT CTA AGT ACA 470
Val Val Arg Pro Thr Arg Lys Lys Thr Leu Ser Thr
 5 10 15

```

## (2) INFORMATION FOR SEQ ID NO: 213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 4..55
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 19..70



id T18977  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 141..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 157..211  
id T18977  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 92..137  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 109..154  
id T18977  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 245..355  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..111  
id HSC12A111  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 321..355  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..35  
id W73324  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 133..345  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.6  
seq VVXFLLLLAXLIA/TY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

```
AAGCAGCTTC CAGGATCCTG AGATCCGGAG CAGCCGGGGT CGGAGCGGCT CCTCAAGAGT 60
TACTGATCTA TNNATGGCAG AGAAAAAAAA ATTGTGACCA GAGACGTGTA GCAATGAACA 120
AGGAACRTCA TA ATG RWN NNK TTC ACA GAC CCC TCT TCA GTG AAT GAA AAG 171
 Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys
 -70 -65 -60

AAG AGG AGG GAG CGG GAA GAA AGG CAG AAT ATT GTC CTG TGG AGA CAG 219
Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln
 -55 -40 -45
```

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CCG CTC ATT ACC TTG CAG TAT TTT TCT CTG GAA ATC CTT GTA ATC TTG | 267 |
| Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu |     |
| -40 -35 -30                                                     |     |
| AAG GAA TGG ACC TCA AAA TTA TGG CAT CGT CAM MGC ATT GTG GTG WCT | 315 |
| Lys Glu Trp Thr Ser Lys Leu Trp His Arg Xaa Xaa Ile Val Val Xaa |     |
| -25 -20 -15                                                     |     |
| TTT TTA CTG CTG CTT GGT DGG CTT ATA GCT ACG TAT TAT             | 354 |
| Phe Leu Leu Leu Leu Ala Xaa Leu Ile Ala Thr Tyr Tyr             |     |
| -10 -5 1                                                        |     |

AAG GAA TGG ACC TCA AAA TTA TGG CAT CGT CAM MGC ATT GTG GTG WCT 315  
Lys Glu Trp Thr Ser Lys Leu Trp His Arg Xaa Xaa Ile Val Val Xaa  
-25 -20 -15

TTT TTA CTG CTG CTT GGT DGG CTT ATA GCT ACG TAT TAT 354  
Phe Leu Leu Leu Leu Ala Xaa Leu Ile Ala Thr Tyr Tyr  
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 189..311  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 75..197  
id AA021160  
est

(1K) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 249..293  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.6  
seq LLRGLLWXQVLCA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACCTTTCTGG GTTGAGCATG GCTGAAGTGA CTCAGCCCAT GGGAGGTTTC CTAGGAGNAA | 60  |
| CAGGCTCCAC TTGCTGCCTC TCTGCGTGAA CTCGGTGTGC CGGCAACCTG GCGACCAGAC | 120 |
| TCCTGCCTTC GGAGGGGCTG GGGCTCCAGG ACGTGAGTGC CCCCCRNKGT TGGAAGGCGG | 180 |
| TGTCATATGT GCACAGAAGC CAAAAAGCAT TGCTGGTATT TCGAAGGACT CTATCCAACC | 240 |
| YHPTATAT ATG CCG CTC CTA CGA GGA CTG CTG TGG STC CAG GTG CTG TGT  | 290 |
| Met Pro Leu Leu Arg Gly Leu Leu Trp Xaa Gln Val Leu Cys           |     |
| -15 -10 -5                                                        |     |
| GGG GGC CCT CTC CAT ACA GAG                                       | 311 |
| Ala Gly Pro Leu His Thr Glu                                       |     |

CAGGCTCCAC TTGCTGCCTC TCTGCGTGAA CTCCTGTGTC CGGCAACCTG GCGACCAGAC 120

TCCTGCCTTC GGAGGGGCTG GGGCTCCAGG ACCTGAGTGC CCCCCRNKGT TGGAAGGCGG 180

TGTCATATGT GCACAGAAGC CAAAAGCAT TGCTGGTATT TCGAAGGACT CTATCCAACC 240

YHPTATAT ATG CCG CTC CTA CGA GGA CTG CTG TGG STC CAG GTG CTG TGT 290  
Met Pro Leu Leu Arg Gly Leu Leu Trp Xaa Gln Val Leu Cys  
-15 -10 -5

GCG GGC CCT CTC CAT ACA GAG 311  
Ala Gly Pro Leu His Thr Glu

1

5

## (2) INFORMATION FOR SEQ ID NO: 215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 31..265  
id T78247  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 6..240  
id W17118  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 11..245  
id N88433  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..336
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 32..247  
id R35014  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 9..217  
id AA074562

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 159..218
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.4  
seq AVVGGCLLVPPAEA/NK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

```

AAGAGGCGGA GATGGCGGAG GGCGGTGGGA CGTGATGCGC GGGTCAGAGC CGGGCCTTGA 60
GAAGGAACTG GAGGCCCTTG GCAGCGGTGT CCCCTCGAGG ACCCCTCTGC CGGGCTCACC 120
AGGTGTCCGG CTTTGCTGGC CCAGCAAGCC TGATAAGC ATG AAG CTC TTA TCT TTG 176
 Met Lys Leu Leu Ser Leu
 -20 -15

GTG GCT GTG GTC GGG TGT TTG CTG GTG CCC CCA GCT GAA GCC AAC AAG 224
Val Ala Val Val Gly Cys Leu Leu Val Pro Pro Ala Glu Ala Asn Lys
 -10 -5 1

AGT TCT GAA GAT ATC CRG TGC AAA TGC ATC TGT CCA CCT TAT AGA AAC 272
Ser Ser Glu Asp Ile Xaa Cys Lys Cys Ile Cys Pro Pro Tyr Arg Asn
 5 10 15

ATC AGT GGG CAC ATT TAC AAC CAG AAT GTA TCC CAG AAG GAC TGC AAC 320
Ile Ser Gly His Ile Tyr Asn Gln Asn Val Ser Gln Lys Asp Cys Asn
 20 25 30

TGC CTG CAC GTG GTG GAG CCC ATG CCA GTG CCG 353
Cys Leu His Val Val Glu Pro Met Pro Val Pro
 35 40 45

```

## (2) INFORMATION FOR SEQ ID NO: 216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 15..332  
id HUM085F04B  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 139..249  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 187..297  
id H85714  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 249..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 295..368  
id H85714  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 86..148  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 133..195  
id H85714  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 135..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 80..264  
id R77008  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 86..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 94..327  
id H49758  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 135..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 53..237  
id AA056366  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 114..185  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

```

AATTGGCTGG CTCTGSAAGC GCAGGTGGTC CTTCTTCTAC TGTCACATGG TGC GCGCTGT 60
TTTCTAATCA CGKGGGTGCC ACCCAGGCCT CTCTGCTCCT GTCKTKTGTT TGG ATG 116
 Met
CCG GCG CTG CTG CCT GTG GCC TCC CGC CTT TTG TTG CTA CCC CGA GTC 164
Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val
 -20 -15 -10
TTG CTG ACC ATG GCC TCT GGA AGC CCT CCG ACC CAG CCC TCG CCG GCC 212
Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala
 -5 1 5
TCG GAT TCC GGC TCT GGC TAC GTT CCG GGC TCG GTC TCT GCA GCC TTT 260
Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val Ser Ala Ala Phe
 10 15 20 25
GTT ACT TGC CCC AAC GAG AAG GTC GCC AAG GAG ATC GCC AGG GCC GTC 308
Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile Ala Arg Ala Val
 30 35 40
GGG GAG AAG CCG 320
Gly Glu Lys Arg
 45

```

## (2) INFORMATION FOR SEQ ID NO: 217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..381
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 73..333  
id H95186  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 72..133
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 25..86  
id H95186  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 28..351
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLGLLSAEQLAEA/SV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

```

ACGGGTGCCG GGTGGAGCGA ASACGGA ATG TGT CTC CTG CTG GGG GCC ACG GGC 54
 Met Cys Leu Leu Leu Gly Ala Thr Gly
 -105 -100

GTC GGG AAG ACG CTG CTG GTG AAA CGG CTG CAG GAG GTG AGC TCC CGG 102
Val Gly Lys Thr Leu Leu Val Lys Arg Leu Gln Glu Val Ser Ser Arg
 -95 -90 -85

GAT GGG AAA GGC GAC CTG GGG GAG CGG CCC CGG ACA CGG CCC ACG GTG 150
Asp Gly Lys Gly Asp Leu Gly Glu Pro Pro Pro Thr Arg Pro Thr Val
 -80 -75 -70

GGC ACC AAT CTT ACT GAC ATC GTG GCA CAG AGA AAG ATC ACC ATC CGG 198
Gly Thr Asn Leu Thr Asp Ile Val Ala Gln Arg Lys Ile Thr Ile Arg
 -65 -60 -55

GAG CTT GGG GGG TGC ATG GGC CCC ATC TGG TCC AGT TAC TAT GGA AAC 246
Glu Leu Gly Gly Cys Met Gly Pro Ile Trp Ser Ser Tyr Tyr Gly Asn
 -50 -45 -40

TGC CGT TCT CTC CTG TTT GTG ATG GAC GCC TCT GAC CCC ACC CAG CTC 294
Cys Arg Ser Leu Leu Phe Val Met Asp Ala Ser Asp Pro Thr Gln Leu
 -35 -30 -25 -20

TCT GCA TTM SGT GTG CAG CTC TTA GGT CTC CTT TCT GCA GAA CAA CTT 342
Ser Ala Xaa Xaa Val Gln Leu Leu Gly Leu Leu Ser Ala Glu Gln Leu
 -15 -10 -5

GCA GAA GCA TCG GTG CTG ATA CTC TTC AAT AAA ATC GAC AAC 384
Ala Glu Ala Ser Val Leu Ile Leu Phe Asn Lys Ile Asp Asn
 - 1 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 94..197  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 92..195  
id T93931  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 2..45  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..44  
id T93931  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 53..97  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 52..96  
id T93931  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 190..234  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 187..231  
id T93931  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 138..196  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 241..299  
id N25481  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 190..234  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 292..336  
id N25481  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 94..211  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 65..182  
id W19370  
est



## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 94..196  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 56..158  
id N35539  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 190..234  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 151..195  
id N35539  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 56..97  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 19..60  
id N35539  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 94..193  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 96..195  
id W87436  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..49  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 7..54  
id W87436  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 75..197  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.7  
seq LLCLGQLHHPGLG/RV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

```
AAAGTTTGTT CCCCAGATTG GGAGCCTAGG AGCCCCCGGC GGCTGCGGCG CAGGTGCCCT 60
CGGCCTTAGT CGGG ATG GAG CTG CCT GCK GTG AAC CTT GAA AGT GAT TCT 110
Met Glu Leu Pro Ala Val Asn Leu Glu Ser Asp Ser
-40 -35 -30
```

```

CCT AGG TCA CTG GCT GCT GAC AAC CTG GGG CTG CAT TGT ATT CTC AGG 158
Pro Arg Ser Leu Ala Ala Asp Asn Leu Gly Leu His Cys Ile Leu Arg
 -25 -20 -15

CTC CTA TGC CTG GGC CAA CTT CAC CAT CCT GGC CTT GGG CGT GTG GGC 206
Leu Leu Cys Leu Gly Gln Leu His His Pro Gly Leu Gly Arg Val Gly
 -10 -5 1

TGT GGC TCA GCG GGA CTC CAT CGA CGC CGG 236
Cys Gly Ser Ala Gly Leu His Arg Arg Arg
 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..240
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 99..194  
id N28787  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..95  
id N28787  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 207..280  
id N28787  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 114..208

WO 99/06550

198

id AA102327  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 59..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 30..110  
id AA102327  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 31..63
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..33  
id AA102327  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 277..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 250..284  
id AA102327  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..240
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 101..196  
id AA019783  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 209..282  
id AA019783  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 37..97  
id AA019783  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 145..240
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95  
region 115..210  
id AA059290  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 41..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 13..111  
id AA059290  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 253..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 223..289  
id AA059290  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 145..240  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 102..197  
id H86516  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 253..326  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 210..283  
id H86516  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 75..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 34..98  
id H86516  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 171..323  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.6  
seq PALILLFALGSLG/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

AGGTCTTCCT CCGGGAAGTG CCGAGGAGGC GGTTCGGTT AGTGGACCGG GACCGGTAGG 60

```

GGTCCTGTTG CCATCATGGC TCACCCCGAC CCCCCTAGC CTCGCTCCTC GATCGAGGAC 120
GACTTCAACT ATGGCAGCAA GCGTKGGCYT CAGGACCGT GCACATCCGA ATG GCC 176
 Met Ala
 -50

TTT CTG AGA AAA GTC TAC AGC ATT CTT TCT CTG CAG GTT CTC TTA ACT 224
Phe Leu Arg Lys Val Tyr Ser Ile Leu Ser Leu Gln Val Leu Leu Thr
 -45 -40 -35

ACA GTG ACT TCA ACA GTT TTT TTA TAC TTT GAG TCT GTA CGG ACA TTT 272
Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Gln Ser Val Arg Thr Phe
 -30 -25 -20

GTA CAT GAG AGT CCT GCC TTA ATT TTG CTG TTT GCC CTC GGA TCT CTG 320
Val His Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly Ser Leu
 -15 -10 -5

GGT TCG GGG 329
Gly Ser Gly
1

```

## (2) INFORMATION FOR SEQ ID NO: 220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..202
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..180  
id W88492  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 25..111
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq PTLAIALAANAWA/FV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

```

ACCATATGGG TGGTGTGGAT CGTC ATG TAT ACT TAC GGC AAC AAG CAG CAC 51
Met Tyr Thr Tyr Gly Asn Lys Gln His
 -25

```

```

AAC AGT CCC ACC TGG GAT GAC CCC ACG CTG SCC ATC GCC CTC GCC GCC 99
Asn Ser Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile Ala Leu Ala Ala
-20 -15 -10 -5

AAT GCC TGG GCC TTC GTC CTC TTC TAC GTC ATC CCC GAG GTC TCC CAG 147
Asn Ala Trp Ala Phe Val Leu Phe Tyr Val Ile Pro Glu Val Ser Gln
 1 5 10

GTG ACC AAG TCC AGC CCA GAG CAA AGC TAC CAG GGG GAC ATG TAC CCC 195
Val Thr Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly Asp Met Tyr Pro
 15 20 25

ACC CGG GAC TTG 207
Thr Arg Asp Leu
 30

```

## (2) INFORMATION FOR SEQ ID NO: 221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(136..167)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 239..270  
id H62766  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 70..165
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq WILVLALPLTVWP/WL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

```

ACTTTCAGTT TCCTTCTTCC AGCACGGAGT ACACTGCTCT GCCTCCACTT AGATTACTTC 60

AGAAATGAA ATG CAG CAA ATA TTT ATC CAG CAG TGC AGG GAG TTG AAC TTT 111
Met Gln Gln Ile Phe Ile Gln Gln Cys Arg Glu Leu Asn Phe
-30 -25 -20

TGG AST CGG GAA CCT TGG ATT CTT GTT CTG SCT CTG CCA CTT ACT GTG 159
Trp Ser Arg Glu Pro Trp Ile Leu Val Leu Ala Leu Pro Leu Thr Val
-15 -10 -5

```

TGG CCT TGG CTC TCC CCG GAG GCT CAG CCC GGT CTG  
Trp Pro Trp Leu Ser Pro Glu Ala Gln Pro Pro Leu  
1 5 10

195

## (2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 308..370  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 404..466  
id AA153879  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 110..154  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.5  
seq AVLLALLMAGLAL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

AACTGGGTCC AGGAAACCCG CTGGTGTGTA CTGTGGGCAG TCCAGCCTCT CCCCATTGTA 60

GGCCATATAA ANNACCTGAG GCCCTCTCCA CCACAGCCCA CCAGTGACC ATG AAG GCT 118  
Met Lys Ala  
-15

GTG CTG CTT GCC CTG TTG ATG GCA GGC TTG GCC CTG CAG CCA GGC ACT 166  
Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln Pro Gly Thr  
-10 -5 1

GCC CTG CTG TGC TAC TCC TGG ARR GCC CAG GTG RGC AAC GAG GAC TGC 214  
Ala Leu Leu Cys Tyr Ser Trp Xaa Ala Gln Val Xaa Asn Glu Asp Cys  
5 10 15 20

CTG CAG GTG GAG AAC TGC ACC CAG CTG GGG GAG CAG TGC TGG ACC GCG 262  
Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys Trp Thr Ala  
25 30 35

CGC ATC CGC GCA GTT GGC CTC CTG ACC GTC ATC AGC AAA GGC TGC AGC 310  
Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys Gly Cys Ser  
40 45 50

TTG AAC TGC GTG GAT SAC TCA CAG GAC TAC TAC GTG GGC AAG AAG AAC 358  
 Leu Asn Cys Val Asp Xaa Ser Gln Asp Tyr Tyr Val Gly Lys Lys Asn  
           55                                60                                65

ATC ACG TGC TGT GAC 373  
 Ile Thr Cys Cys Asp  
           70

## (2) INFORMATION FOR SEQ ID NO: 223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
                           region 1..247  
                           id AAL66578  
                           est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 4..51
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1  
                           seq QACLLGLFALILS/GK

## -(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

AGA ATG GGA CTC CAA GCC TGC CTC CTA GGG CTC TTT GCC CTC ATC CTC 48  
 Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu  
       -15                                -10                                -5

TCT GGC AAA TGC AGT TAC AGC CCG GAG CCC GAC CAG CGG AGG ACG CTG 96  
 Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr Leu  
       1                                5                                10                                15

CCC CCA GGC TGG GTG TCC CTG GGC CGT GCG GAC CCT GAG GAA GAG CTG 144  
 Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu Glu Leu  
                                 20                                25                                30

AGT CTC ACC TTT GCC CTG AGA CAG CAG AAT GTG GAA AGA CTC TCG GAG 192  
 Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg Leu Ser Glu  
                                 35                                40                                45

CTG GTG CAG GGT GTG TCG GAT CCC AGC TCT CCT CAA TAC CGA AAA TAC 240



Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln Tyr Gly Lys Tyr  
50 55 60

CTG ACC GGT

249

Leu Thr Arg

65

## (2) INFORMATION FOR SEQ ID NO: 224:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(141..361)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 146..366  
id H19708  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 143..264  
id H20045  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 4..77  
id H20045  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 8..247  
id C15772  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 157..341  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 1..185  
                           id H67240  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 340..382  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 185..227  
                           id H67240  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 172..382  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 1..211  
                           id HUM408E11B  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 2..88  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7  
                           seq LGSGGLGLSPGTSS/GR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| G ATG AGG CCG GGG CAG GTC TCC CTC CTG GGT CCT GAT GCT GTT TCT GTG | 49  |
| Met Arg Pro Gly Gln Val Ser Leu Leu Gly Pro Asp Ala Val Ser Val   |     |
| -25 -20 -15                                                       |     |
| CTC GGC TCT GGC TTG GGC CTC AGC CCT GGC ACC AGC TCT GGC CGC AAC   | 97  |
| Leu Gly Ser Gly Leu Gly Leu Ser Pro Gly Thr Ser Ser Gly Arg Asn   |     |
| -10 -5 1                                                          |     |
| CCT GAC CCT GGC TCT GGG CCG GGC ACT CTG CCG GRT YCC AGC DTC CAA   | 145 |
| Pro Asp Pro Gly Ser Gly Pro Gly Thr Leu Pro Xaa Xaa Ser Xaa Gln   |     |
| 5 10 15                                                           |     |
| AGC CCC TCC CCG GCT CCA GAT CCA CCC CCA GCC CTA CTC CTG TGG AAT   | 193 |
| Asn Pro Ser Pro Ala Pro Asp Pro Pro Pro Ala Leu Leu Leu Trp Asn   |     |
| 20 25 30 35                                                       |     |
| CTT CTG ACC CAA AGG CTG GGC ACG ACG CTG CTC CCG ACC TTG TGC CCA   | 241 |
| Leu Leu Thr Gln Arg Leu Gly Thr Thr Leu Val Pro Thr Leu Cys Pro   |     |
| 40 45 50                                                          |     |
| GGC CAG ACC TTG ATC CTG TGC CCA GCC CAG ACC CTG ATC CTG TGC CCA   | 289 |
| Ala Gln Thr Leu Ile Leu Cys Pro Ala Gln Thr Leu Ile Leu Cys Pro   |     |
| 55 60 65                                                          |     |
| ACC CTG ATC CCA ACC CTG TGT CCT GCC CTG ACC CCT GTT CTC CCA CTC   | 337 |
| Xaa Leu Ile Pro Thr Leu Cys Pro Ala Leu Xaa Pro Val Leu Pro Xaa   |     |

|                                                             |    |    |     |
|-------------------------------------------------------------|----|----|-----|
| 70                                                          | 75 | 80 |     |
| GTG GCA CTG TCA GCC CAG CCC TCC CTA CCG GCG AGA GTC CAG AGT |    |    | 382 |
| Val Ala Leu Ser Ala Gln Pro Ser Leu Pro Ala Arg Val Gln Ser |    |    |     |
| 85                                                          | 90 | 95 |     |

## (2) INFORMATION FOR SEQ ID NO: 225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..139)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 135..272  
id HSB82C022  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 10..108
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8  
seq FTSASLLLPMTG/MP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATTATTTAT ATG ATT AAC CCC TCA GTC CCT AGC AAG TCA AAT TCC CAT CCG | 51  |
| Met Ile Asn Pro Ser Val Pro Ser Lys Ser Asn Ser His Pro           |     |
| -30 -25 -20                                                       |     |
| TTT TTA TCT ACA GTA ATG TTC ACC TCT GCA TCA CTG CTG CTT CCC ATG   | 99  |
| Phe Leu Ser Thr Val Met Phe Thr Ser Ala Ser Leu Leu Leu Pro Met   |     |
| -15 -10 -5                                                        |     |
| TCT ACA GGC ATG CCA ACT CAA AAC TGT TTT ACC CCA AAG               | 138 |
| Ser Thr Gly Met Pro Thr Gln Asn Cys Phe Thr Pro Lys               |     |
| 1 5 10                                                            |     |

## (2) INFORMATION FOR SEQ ID NO: 226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 138..186

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 91  
region 14..62  
id AA111755  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 83..286

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.7  
seq IACLAWWIGGGSG/XN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

```

AAAGACTTTG CGAASGCTGC GCTCGCGCCC GGATCCCTCA GCGGCTGCA GCCTTCAGCC 60
TGCCTGGTT GGTGAAACAG AG ATG TCA GAA AAG GAG AVC AAC TTC CCG CCA 112
 Met Ser Glu Lys Glu Xaa Asn Phe Pro Pro
 -65 -60

CTG CCC AAG TTC ATC CCT GTG AAG CCC TGC TTC TAC CAG AAC TTC TCC 160
Leu Pro Lys Phe Ile Pro Val Lys Pro Cys Phe Tyr Gln Asn Phe Ser
 -55 -50 -45

GAC GAG ATC CCA GTG GAG CAC CAG GTC CTG GTG AAG AGG ATC TAC CGG 208
Asp Glu Ile Pro Val Glu His Gln Val Leu Val Lys Arg Ile Tyr Arg
 -40 -35 -30

CTG TGG ATG TTT TAC TGC GCC ACC CTC GGC GTC AAC CTC ATT GCC TGC 256
Leu Trp Met Phe Tyr Cys Ala Thr Leu Gly Val Asn Leu Ile Ala Cys
 -25 -20 -15

CTG GCC TGG TGG ATC GGC GGA GGC TCG GGG NNB AAC TTC GGC CTG GCC 304
Leu Ala Trp Trp Ile Gly Gly Gly Ser Gly Xaa Asn Phe Gly Leu Ala
 -10 -5 1 5

TTC GTG TGG CTG CTC CTG TTC ACG CCT TGC GGC TAC GTG TGC TGG TTC 352
Phe Val Trp Leu Leu Leu Phe Thr Pro Cys Gly Tyr Val Cys Trp Phe
 10 15 20

GGG CCT GTC TAC AAG GCC TTC CGA GCC GAC AGC TCC TTT AAT TTC ATG 400
Arg Pro Val Tyr Lys Ala Phe Arg Ala Asp Ser Ser Phe Asn Phe Met
 25 30 35

GGG CTG
Ala Leu
 40

```

406

## (2) INFORMATION FOR SEQ ID NO: 227:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(68..131)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 392..455  
id W22335  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 288..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 9..68  
id H70453  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 159..227
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq ILRLYFFLQLAHS/GY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

```

ACGAAATGGT ATTGACATCT TGSTTGAAC ACCTGGTCGT ATCAAAGACC ATCTGCAGAG 60
TGGCCGATTG GATCTTTCTA AACTGCGACA TGTTGTGCTT GATGAAGTGG ATCAGATGTT 120
AGATTTAGGT TTCGCTGAAC AAGTTGAAGA TATTATTC ATG AAT CCT ACA AAA CTC 176
 Met Asn Pro Thr Lys Leu
 -20

ATT CTG AAG ACA ATC CTC AGA CTT TAC TTT TTT CTG CAA CTT GCC CAC 224
Ile Leu Lys Thr Ile Leu Arg Leu Tyr Phe Phe Leu Gln Leu Ala His
 -15 -10 -5

AGT GGG TAT ACA AAG TTG CAA AAA AAA TAC ATG AAA TCC AGA TAT GAA 272
Ser Gly Tyr Thr Lys Leu Gln Lys Lys Tyr Met Lys Ser Arg Tyr Glu
 1 5 10 15

CAG GTT GAG CTT GTT GGR AAA ATG WCT CAA AAG GCT GCA AAT ACT GTG 320

```

Gln Val Asp Leu Val Gly Lys Met Xaa Gln Lys Ala Ala Thr Thr Val  
20 25 30  
GRA CAT TTG GCC ATC CAG TGT CAT TGG 347  
Xaa His Leu Ala Ile Gln Cys His Trp  
35 40

## (2) INFORMATION FOR SEQ ID NO: 228:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..70
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..59  
id AA013305  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 197..250
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 189..242  
id AA013305  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 250..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 243..290  
id AA013305  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..199
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 236..299  
id R48472  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 37..101  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 135..199  
                           id R48472  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 38..106  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.7  
                           seq SXXCFVSVPPASA/IP

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

```

AACCCGGGAC CGAGCTGGGG TCTTGAGGA AGAGAGG ATG GCG TCG TCG AGC CCT 55
 Met Ala Ser Ser Ser Pro
 -20

GAC TCC CCA TGT TCC TGS NAC TGC TTT GTC TCC GTG CCC CCG GGC TCA 103
Asp Ser Pro Cys Ser Xaa Xaa Cys Phe Val Ser Val Pro Pro Ala Ser
 -15 -10 -5

GCC ATC CCG GST GTG AKC TTK GCC NNH AAC TCG GAC SGA CCC CCG GAC 151
Ala Ile Pro Xaa Val Xaa Xaa Ala Xaa Asn Ser Asp Xaa Pro Arg Asp
 1 5 10 15

GAG GTG CAG GAG GTG GTG TTT GTC CCC GCA GGC ACT CAC ACT CCT GGG 199
Glu Val Gln Glu Val Val Phe Val Pro Ala Gly Thr His Thr Pro Gly
 20 25 30

AGC CGG CTC CAG TGC ACC TAC ATT GAA GTG GAA CAG GTG TCG AAG ACG 247
Ser Arg Leu Gln Cys Thr Tyr Ile Glu Val Glu Gln Val Ser Lys Thr
 35 40 45

CAC GGT GTG ATT CTG AGC CGT CCT TCT TGG CTA TGG GGG GCT GAG ATG 295
His Ala Val Ile Leu Ser Arg Pro Ser Trp Leu Trp Gly Ala Glu Met
 50 55 60

GGC GMV ACG AGC ATG GTG TCT GCA TTG GCA ACG AGG CTG TGT GGA CGA 343
Gly Xaa Thr Ser Met Val Ser Ala Leu Ala Thr Arg Leu Cys Gly Arg
 65 70 75

AGG AGC CAG TTG GGG AGG GCN GKN GCC CTS CTG GGC ATG GAC CTA CTC 391
Arg Ser Gln Leu Gly Arg Ala Xaa Ala Leu Leu Gly Met Asp Leu Leu
 80 85 90 95

AGG TGC AGA CCC TGC 406
Arg Cys Arg Pro Cys
 100

```

## (2) INFORMATION FOR SEQ ID NO: 229:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 128..197

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 158..227  
id AA249540  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 241..309

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92  
region 267..335  
id AA249540  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 164..240

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 58..134  
id N46699  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 128..161

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 23..56  
id N46699  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(224..309)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96  
region 104..189  
id W39777  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 233..309

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96  
region 13..89  
id AA036848  
est



## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 233..309  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 13..89  
                           id AA133513  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 171..287  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.7  
                           seq XLIAXLEPPGAMA/VR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

```

CATTATTCCT TTTCCATCGG AAGTGGCGCT CGTGCATTCA ACTTGTTCCC GTCATGGAA 60
CCCCTCTTTA AAAAGACGCA GGGCACCTGT GAGCGCAGGA GCGAGCCTAA GGCCACCCAG 120
CGGCAGCGCC CGTGTCTTGG GCACTCAGCG TGCTGGGCAG AGCAGGTGCG ATG GSC 176
 Met Xaa
CCA GTC CTA GCA GCC CTC GCC CAT GTC CTG TGC CCT TAC ATG GCT CCC 224
Pro Val Leu Ala Ala Leu Ala His Val Leu Cys Pro Tyr Met Ala Pro
 -35 -30 -25
GGA CTG TGC AGG GAG CCG ATA CGT TTK CTG ATA GCA VTA CTG GAA CCA 272
Gly Leu Cys Arg Glu Pro Ile Arg Xaa Leu Ile Ala Xaa Leu Glu Pro
 -20 -15 -10
CCG GGT GCG ATG GCA GTK AGG AGA CTG CCC AGT GCC 308
Pro Gly Ala Met Ala Val Arg Arg Leu Pro Ser Ala
 -5 1 5

```

## (2) INFORMATION FOR SEQ ID NO: 230:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 19..327  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 1..309

id C16848  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 75..104  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 303..332  
id R40385  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 73..207  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq PMLGLAAFRWIWS/RE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

```

AAAAGCGGAC CCGCGGACGG TGGCGTTAAG GGAACGCTGA GGTCCCGCGC TCCCCGACCG 60
AGGTATATCT CC ATG AAT AAC CTA AAT GAT CCC CCA AAT TGG AAT ATC CGG 111
 Met Asn Asn Leu Asn Asp Pro Pro Asn Trp Asn Ile Arg
 -45 -40 -35

CCT AAT TCC AGG GCG GAT GGT GGT GAT GGA AGC AGG TGG AAT TAT GCC 159
Pro Asn Ser Arg Ala Asp Gly Gly Asp Gly Ser Arg Trp Asn Tyr Ala
 -30 -25 -20

CTG TTG GTT CCA ATG CTG GGA TTG GCT GCT TTT CGT TGG ATT TGG TCT 207
Leu Leu Val Pro Met Leu Gly Leu Ala Ala Phe Arg Trp Ile Trp Ser
 -15 -10 -5

AGG GAG TCC CAG AAA GAA GTA GAA AAA GAG AGA GAA GCC TAC CGT CGG 255
Arg Glu Ser Gln Lys Glu Val Glu Lys Glu Arg Glu Ala Tyr Arg Arg
 1 5 10 15

AGA ACT GCT GCT TTT CAA CAG GAT CTG GAA GCC AAG TAC CAC GCC ATG 303
Arg Thr Ala Ala Phe Gln Gln Asp Leu Glu Ala Lys Tyr His Ala Met
 20 25 30

ATC TCA GAM AAT CGG CGT GCT GTC 327
Ile Ser Xaa Asn Arg Arg Ala Val
 35 40

```

## (2) INFORMATION FOR SEQ ID NO: 231:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (11) MOLECULE TYPE: CDNA

## (12) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(3..297)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..295  
id W57719  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(37..300)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 10..273  
id H04979  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(7..41)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 270..304  
id H04979  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(37..295)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 7..265  
id H10390  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..41)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 262..301  
id H10390  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(142..295)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..154  
id W42765  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..141)  
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 156..295  
id W42765  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(55..238)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 71..254  
id R39116  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(255..297)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 10..52  
id R39116  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 295..351  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.6  
seq AALCSLFFFLSLQ/EI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

```

ACGTTAGGGG GCCAGGGAGA TGTGACTGAG GCTGGCTTTC CACGTGAATC AGACGGGGTC 60
GGTGGAGGGT TTGGTGCTAC AGCCAGTCAG AAGATTTGCA AATGCGAACA CATTCCTGTG 120
TGAGGCACGT TACCCTTTGT CAGTTATTGT GAATATGTGT ATTTTAAGCA ATAAGATTCA 180
GCTGGTCAGA CTTTTCTGGG CAGTCTCAGT GACGCATTTC CTGTGCTGTG ATTGTCTGTA 240
AGACAGAGTG GCTCTAACCA CTGTGAGAAG CCCAAATAAA AATTGATCCC AAAA ATG 297
 Met
CTA CTG CTC TTT CTT GCT GCA CTT TGT TCC CTC TTC TTC TTC CTC AGT 345
Leu Leu Leu Phe Leu Ala Ala Leu Cys Ser Leu Phe Phe Phe Leu Ser
 -15 -10 -5

CTT CAG GAA ATT GCA CCT CAA GAT CCC AAA CCA GGG 381
Leu Gln Glu Ile Ala Pro Gln Asp Pro Lys Pro Gly
 1 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 232:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 17..175

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 91  
region 1..159  
id W51023  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 42..173

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 1..132  
id T61976  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 2..142

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.5  
seq IIVCLFAFLVAHC/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

```
T ATG TTA TTC CTT GGC AAG GTG CTG ATA GTC TGC AGC ACA GGT TTA GCT 49
Met Leu Phe Leu Gly Lys Val Leu Ile Val Cys Ser Thr Gly Leu Ala
 -45 -40 -35

GGG ATT ATG CTG CTC AAC TAC CAG CAG GAC TAC ACA GTA TGG GTG CTG 97
Gly Ile Met Leu Leu Asn Tyr Gln Gln Asp Tyr Thr Val Trp Val Leu
 -30 -25 -20

CCT CTG ATC ATC GTC TGC CTC TTT GCT TTC CTA GTC GCT CAT TGC TTC 145
Pro Leu Ile Ile Val Cys Leu Phe Ala Phe Leu Val Ala His Cys Phe
 -15 -10 -5 1

CTG TCT ATT TAT GAA ATG GTA GTC GAT GCG AGG 178
Leu Ser Ile Tyr Glu Met Val Val Asp Ala Arg
 5 10
```

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..321)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 59..378  
id AA045815  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..244
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..150  
id R18658  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 240..321
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 147..228  
id R18658  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..321
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..227  
id R14615  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..200)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 3..201  
id N95174  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(36..197)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 8..169  
id N93742  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..44)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 166..208  
id N93742  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 191..304  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq LLLLVHSFWFTVC/TP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

```
AAGACTCATA GAGATTAAAT GATCACTATG GTCCTCTTTC TGTAAATGG AGCCAAAGAC 60
GCCTATGTTG TTCTGAAGTC TTGTAATGTT TAACTTCTGA GAACTTAGAT TAGTGGTGTG 120
ATGATAGAGT CTGTATAACG CATTGAAAAG GGTATCAGGC TTAGTTATTT ATCCAATAAA 180
TATTTATTGT ATG CAG GGT ATT CCT ATT TTA ACT CCT GTG ACA ACA CAA 229
 Met Gln Gly Ile Pro Ile Leu Thr Pro Val Thr Thr Gln
 -35 -30

AGC ATA GCG ATT TCC ATA GTT CTA ACT GTT CAG GGT CTG CTC CTC CTG 277
Ser Ile Ala Ile Ser Ile Val Leu Thr Val Gln Gly Leu Leu Leu Leu
-25 -20 -15 -10

GTA CAC TCT TTT TGG TTC ACT GTA TGT ACT CCT GTT GTC TTT 319
Val His Ser Phe Trp Phe Thr Val Cys Thr Pro Val Val Phe
 -5 1 5
```

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(131..360)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 45..274  
id M78402  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(57..234)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 10..187  
id H04786  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(7..43)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 201..237  
id H04786  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(57..234)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 10..187  
id H17078  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(7..43)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 201..237  
id H17078  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(57..217)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..161  
id HSC0UC022  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(1..43)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 175..217  
id HSC0UC022  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 199..279  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq LFCVLLSLRPHTS/GT



(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```

ACAAGATTTT CCAACCTTGC TGGCTACTTT AGTTTGGGAC CTGTTTTTTT TCTCATTTGA 60
TTTTTCCTTGT GCAGAAAATA GTTTCAGCA CATGGATTGA TCTCAGAGAC AATGAGGCTC 120
AGTCTGGGAT AGTCTGTTTT CTCTGAGCAT GTTGGCCAAC TAGTATGGTC AAATTATTGA 180
GTGGATCATC TCTTGGAA ATG CAG AAC TTC TGC CAC CAC TGG GGT ATT TGC 231
 Met Gln Asn Phe Cys His His Leu Ala Ile Cys
 -25 -20

ACA GTC ATC TTG TTC TGT GTC CTT TTA TCT CTC AGA CCA CAC ACA TCT 279
Thr Val Ile Leu Phe Cys Val Leu Leu Ser Leu Arg Pro His Thr Ser
 -15 -10 -5

GGA ACG CTG TGG GCA TCT TCT GCC CAT GGG CTC CAT TTG GCA CCT GCT 327
Gly Thr Leu Trp Ala Ser Ser Ala His Gly Leu His Leu Ala Pro Ala
 1 5 10 15

GAG CCA CAG TTG TCC TGC TGG ATG TGC TGT GCA 360
Glu Pro Gln Leu Ser Cys Trp Met Cys Cys Ala
 20 25

```

(2) INFORMATION FOR SEQ ID NO: 235:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 35..326  
id H97426  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 92..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 14..238  
id W44834  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 127..177  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 4..54  
 id R57989  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 182..211  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 62..91  
 id R57989  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(287..316)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 385..414  
 id N93806  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 34..225  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.3  
 seq VLMRLVASAYSIA/QK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| AAGTTTCCCG CATGCTCAGT AGCTGAGGTA GGG ATG CCA TCC TTC TCA AAA GAC | 54  |
| Met Pro Ser Phe Ser Lys Asp                                      |     |
| -60                                                              |     |
| TTA TTG ACA GTG CCA AAG CTC GGT ACT GGA CAC VMC GRR GGR MCT GGG  | 102 |
| Leu Leu Thr Val Pro Lys Leu Gly Thr Gly His Xaa Xaa Gly Xaa Gly  |     |
| -55 -50 -45                                                      |     |
| TCC TAC GAT RAC GCG CTT KTG CTC CTC CTG AAG TGT CTT TGG TCC AAC  | 150 |
| Ser Tyr Asp Xaa Ala Leu Xaa Leu Leu Lys Cys Leu Trp Ser Asn      |     |
| -40 -35 -30                                                      |     |
| GTT GTT CCA GAG TGT ACC ATG GCT TCC AGT AAC ACT GTG TTG ATG CGG  | 198 |
| Val Val Pro Glu Cys Thr Met Ala Ser Ser Asn Thr Val Leu Met Arg  |     |
| -25 -20 -15 -10                                                  |     |
| TTG GTA GCC TCC GCA TAT TCT ATT GCT CAA AAG GCA GGA ATG ATA GTC  | 246 |
| Leu Val Ala Ser Ala Tyr Ser Ile Ala Gln Lys Ala Gly Met Ile Val  |     |
| -5 1 5                                                           |     |
| AGA CGT GTT ATT GCT GAA GGA GAC CTG GGT ATT GTG GAG AAG ACC TGT  | 294 |
| Arg Arg Val Ile Ala Glu Gly Asp Leu Gly Ile Val Glu Lys Thr Cys  |     |
| 10 15 20                                                         |     |
| GCA ACA GAC CTG CAG ACC AAA GCT GAC CGA TTG GCA CAG ATG AGC ATA  | 342 |
| Ala Thr Asp Leu Gln Thr Lys Ala Asp Arg Leu Ala Gln Met Ser Ile  |     |

|                                                                 |    |    |     |
|-----------------------------------------------------------------|----|----|-----|
| 25                                                              | 30 | 35 |     |
| TGT TCT TCA TTG GYM BGG AAA TTC CCC AAA CTC RNR ATT ATA GGG GAA |    |    | 390 |
| Cys Ser Ser Leu Xaa Xaa Lys Phe Pro Lys Leu Xaa Ile Ile Gly Glu |    |    |     |
| 40                                                              | 45 | 50 | 55  |
| GAG GAT CTG CTT TCT GAG GAA GTG GAT CAA GAG CTG ATT GAA GAC AGK |    |    | 438 |
| Glu Asp Leu Pro Ser Glu Glu Val Asp Gln Glu Leu Ile Glu Asp Xaa |    |    |     |
| 60                                                              | 65 | 70 |     |

## (2) INFORMATION FOR SEQ ID NO: 236:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 15..121  
id W04921  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 114..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 121..227  
id W04921  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 221..310
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 227..316  
id W04921  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(114..213)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 260..353  
id N70602  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(32..113)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 359..440  
id N70602  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(261..311)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 164..214  
id N70602  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(213..259)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 215..261  
id N70602  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 114..194
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 59..139  
id W70167  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 238..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 183..256  
id W70167  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..53  
id W70167  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..236
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 139..182

id W70167  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 221..311  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 165..255  
id W37690  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 114..187  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 58..131  
id W37690  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 56..113  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..58  
id W37690  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 185..220  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 130..165  
id W37690  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 227..289  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.2  
seq LEMXLAFASHIXA/RD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

```

ATGCGACGCTT CCTTGGCTCG GCTTGGTCTG CGGCCTGTCA AACAGGTTTC GGTTCAGTTC 60
TGTCCCTTCG AGAAAAACGT GGAATCGACG AGGACCTTCV TSCAGACGGT GAGGCMGTGA 120
GAAGGTCCGC TCCACTAATC TCAACTGCTC AGTGATTGCG GACGTGASGC ATGACGGCTC 180
CGAGCCCTGC GTGGACGTGC TGTTCCGAGA CGGGCATCGC CIGATT ATG CGC GGC 235
 Met Arg Gly
 -20

GCT CAT CTC ACC GCT CTG GAA ATG CTC ANM GCC TTC GCC TCC CAC ATM 283
Ala His Leu Thr Ala Leu Glu Met Leu Xaa Ala Phe Ala Ser His Ile

```

-15

-10

-5

HGG GCC AGG GAC GCG GCG GGC AGC GGG  
Xaa Ala Arg Asp Ala Ala Gly Ser Gly  
1 5

310

## (2) INFORMATION FOR SEQ ID NO: 237:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 321..431
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 186..296  
id AA043558  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 218..299
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 83..164  
id AA043558  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 39..96  
id AA043558  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..299
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 57..225  
id N50523  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 321..431

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 247..357  
id N50523  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(45..115)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..71  
id N50523  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(321..431)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 289..399  
id AA115605  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(217..318)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 403..504  
id AA115605  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(166..231)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 491..556  
id AA115605  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 172..318  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 36..182  
id AA115129  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 321..431  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 186..296  
id AA115129  
est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 174..318  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 41..185  
                           id AA035548  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 325..431  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 194..300  
                           id AA035548  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 7..423  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.2  
                           seq FGLLHQLSQCVTS/LE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACAAGG ATG GAA GTG GGC TTA CCG GCC ATT ACC CTC TTT CTC ACC AGC  | 43  |
| Met Glu Val Gly Leu Pro Ala Ile Thr Leu Phe Leu Thr Ser         |     |
| -135 -130                                                       |     |
| GCC AGC AGC CCT GTG GTG GCG ACG ACG ATG GAC CAG GAG CCA GTG GGC | 96  |
| Ala Ser Ser Pro Val Val Ala Thr Thr Met Asp Gln Glu Pro Val Gly |     |
| -125 -120 -115 -110                                             |     |
| GGT GTG GAA CGA GGA GAA GCC GTC GCA GCC TCG CGA RCT GCG GCC GCC | 144 |
| Gly Val Glu Arg Gly Glu Ala Val Ala Ala Ser Gly Xaa Ala Ala Ala |     |
| -105 -100 -95                                                   |     |
| GCG GCA TTC GGG GAA TCT GCA GGG CAG ATG AGT AAC GAA AGA GGC TTT | 192 |
| Ala Ala Phe Gly Glu Ser Ala Gly Gln Met Ser Asn Glu Arg Gly Phe |     |
| -90 -85 -80                                                     |     |
| GAA AAT GTA GAA CTG GGA GTC ATA GGA AAA AAG AAG AAA GTC CCA AGG | 240 |
| Glu Asn Val Glu Leu Gly Val Ile Gly Lys Lys Lys Lys Val Pro Arg |     |
| -75 -70 -65                                                     |     |
| AGA GTC ATC CAC TTT GTT AGT GGT GAA ACA ATG GAA GAA TAT AGC ACA | 288 |
| Arg Val Ile His Phe Val Ser Gly Glu Thr Met Glu Glu Tyr Ser Thr |     |
| -60 -55 -50                                                     |     |
| GAT GAA GAC GAA GTT GAT GGC CTG GAG AAG NNG ATG TTT TGC CTA CTC | 336 |
| Asp Glu Asp Xaa Val Asp Gly Leu Glu Lys Xaa Met Phe Cys Leu Leu |     |
| -45 -40 -35 -30                                                 |     |
| TTG ATC CGR CAA AAC TTA CCT GGG GTC CCT ACT TAT GGT TTT ACA TGC | 384 |
| Leu Ile Arg Gln Asn Leu Pro Gly Val Pro Thr Tyr Gly Phe Thr Cys |     |
| -25 -20 -15                                                     |     |
| TTG GGG CTG CTA CAT CAA CTC TCT CAG TGT GTG ACT TCC TTG GAG     | 429 |
| Phe Gly Leu Leu His Gln Leu Ser Gln Cys Val Thr Ser Leu Glu     |     |



-10

-5

1

## (2) INFORMATION FOR SEQ ID NO: 233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 31..251  
id T34679  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 176..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 104..250  
id N34677  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..170
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 21..98  
id N34677  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 190..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 203..335  
id N32531  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 202..334  
id N36824

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 102..170  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 28..96  
                           id N36824  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 175..312  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 100..237  
                           id H97539  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 151..279  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.1  
                           seq SAATLASLGGTSS/RR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

```

AACTCTCGTG CCAAGCATGT CTCTCCAAAT GGCTGCTCTC TGGCGTTCTT CACACTCCCC 60
CTGAAGTTCA TCTAAGATCT TCATTCTTCA WAGGCGGAAG CCCGGCTCGC TGCAAAACGG 120
GCGGCCCGCG CGGAGGCTCG CGAGATCCGC ATG AAG GAG CTG GAG CGG CAG CAG 174
 Met Lys Glu Leu Glu Arg Gln Gln
 -40

AAG GAG GTA GAA GAG AGA CCA GAA AAA GAT TTT ACT GAG AAG GGG TCT 222
Lys Glu Val Glu Glu Arg Pro Glu Lys Asp Phe Thr Glu Lys Gly Ser
-35 -30 -25 -20

CGT AAC ATG CCG GGC CTG TCT GCA GCC ACG CTG GCC TCT CTG GGT GGG 270
Arg Asn Met Pro Gly Leu Ser Ala Ala Thr Leu Ala Ser Leu Gly Gly
 -15 -10 -5

ACT TCC TCT CGG AGA GGC AGC GGA GAC ACC TCC ATC TCC ATC GAC CCC 318
Thr Ser Ser Arg Arg Gly Ser Gly Asp Thr Ser Ile Ser Ile Asp Pro
 1 5 10

GAG
Glu
 321

```

## (2) INFORMATION FOR SEQ ID NO: 239:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 270..403

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92  
region 199..332  
id AAL25491  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 70..135

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93  
region 1..66  
id AAL25491  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(27..135)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 89..197  
id HSB72F052  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(135..223)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 2..90  
id HSB72F052  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 126..188

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.1  
seq VLVLICIVTVCVT/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

```
ACCGGAGAAA AAATGGTTCA TGGAGCCTGC GGTTATIGTT TGCCTGGGTG GAATTTTACC 60
TTTTGGTTCA ATCTTTATPG AAATGTATTT CATCTTCACG TCTTTCTGGG CATATAAGAT 120
CTATT ATG TCT ATG GGC TTC ATG ATG CTG GTG CTG GTT ATC CTG TGC ATT 170
Met Ser Met Gly Phe Met Met Leu Val Leu Val Ile Leu Cys Ile
-20 -15 -10
```

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GTG ACT GTC TGT GTG ACT ATT GTG TGC ACA TAT TTT CTA CTA AAT GCA | 218 |
| Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu Leu Asn Ala |     |
| -5 1 5 10                                                       |     |
|                                                                 |     |
| GAA GAT TAC AGG TGG CAA TGG ACA AGT TTT CTC TCT GGT GCA TCA ACT | 266 |
| Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala Ala Ser Thr |     |
| 15 20 25                                                        |     |
|                                                                 |     |
| GCA ATC TAT GTT TAC ATG TAT TCC TTT TAC TAC TAT TTT TTC AAA ACA | 314 |
| Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe Phe Lys Thr |     |
| 30 35 40                                                        |     |
|                                                                 |     |
| AAG ATG TAT GGC TTA TTT CAA ACA TCA TTT TAC TTT GGA TAT ATG GCG | 362 |
| Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly Tyr Met Ala |     |
| 45 50 55                                                        |     |
|                                                                 |     |
| GTA TTT AGC ACA GCC TTG GGG ATA ATG TGT GGA GCG ATT             | 401 |
| Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile             |     |
| 60 65 70                                                        |     |

## (2) INFORMATION FOR SEQ ID NO: 240:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 153..397
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 131..375  
id W56159  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..121  
id W56159  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 153..467
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 303..617

id HSZ78368  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 60..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 214..293  
id HSZ78368  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 153..374  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 80..301  
id AA026570  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 70..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..70  
id AA026570  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 372..405  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 300..333  
id AA026570  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 155..467  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 83..395  
id AA109961  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 88..139  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 20..71  
id AA109961  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 153..363  
(C) IDENTIFICATION METHOD: blastn

|                                                                 |                                                         |            |            |            |              |  |     |
|-----------------------------------------------------------------|---------------------------------------------------------|------------|------------|------------|--------------|--|-----|
| AACGCTTGCG                                                      | ATGGTTGAAT                                              | TCCCCTCCTC | ACGCCAGCCT | AGGAGAAGAA | GTTTCGTAGTC  |  | 60  |
| CCAGAGGAAG                                                      | AGGAGTTGTA                                              | CGCATGTCAG | AGAGGTTGCA | GGCTGTTTTT | C AATTTGTCAG |  | 120 |
| TTTGTGG                                                         | ATG ATG GAA TTG GRM CTW AAA AKC GRA ACT AAA KKG GAA TGK |            |            |            |              |  | 169 |
|                                                                 | Met Met Glu Leu Xaa Leu Lys Xaa Xaa Thr Lys Xaa Glu Xaa |            |            |            |              |  |     |
| -70                                                             |                                                         |            | -65        |            | -60          |  |     |
| GAA TCT GCA TGT ACA GAA GCA TAT TCC CAA TCT GAT GAG CAA TAT GCT |                                                         |            |            |            |              |  | 217 |
| Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala |                                                         |            |            |            |              |  |     |
| -55                                                             |                                                         |            | -50        |            | -45          |  |     |
| TGC CAT CTT GGT TGC CAG AAT CAG CTG CCA TTC GCT GAA CTG AGA CAA |                                                         |            |            |            |              |  | 265 |
| Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln |                                                         |            |            |            |              |  |     |
| -40                                                             |                                                         |            | -35        |            | -30          |  | -25 |
| GAA CAA CTT ATG TCC CTG ATG CCA AAA ATG CAC CTA CTC TTT CCT CTA |                                                         |            |            |            |              |  | 313 |
| Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu |                                                         |            |            |            |              |  |     |
|                                                                 |                                                         | -20        |            |            | -15          |  | -10 |
| ACT CTG GTG AGG TCA TTC TGG AGT GAC ATG ATG GAC TCC GCA CAG AGC |                                                         |            |            |            |              |  | 361 |
| Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser |                                                         |            |            |            |              |  |     |
|                                                                 | -5                                                      |            |            |            | 1            |  | 5   |
| TTC AKA ACC TCT TCA TGG ACT TTT TAT CTT CAA GCC GAT GMC GGM MAA |                                                         |            |            |            |              |  | 409 |
| Phe Xaa Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Xaa Gly Xaa |                                                         |            |            |            |              |  |     |
| 10                                                              |                                                         |            | 15         |            | 20           |  |     |
| ATA GTT ATA TKC CAG TCT AAG CCA GAA ATC CAG TAC GCA CCA CAT TTG |                                                         |            |            |            |              |  | 457 |
| Ile Val Ile Xaa Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu |                                                         |            |            |            |              |  |     |
| 25                                                              |                                                         |            | 30         |            | 35           |  | 40  |
| GAG CAG GAG                                                     |                                                         |            |            |            |              |  | 466 |
| Glu Gln Glu                                                     |                                                         |            |            |            |              |  |     |

## (2) INFORMATION FOR SEQ ID NO: 241:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..81
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 62..125  
id AA092155  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(18..81)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 68..131  
id AA128307  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(18..81)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 68..131  
id N99068  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(18..81)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 68..131  
id AA039944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(18..81)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 68..131  
id AA128099  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

- (B) LOCATION: 1..72
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq GLILLFASHLINQ/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

ATG GTT TCC AAT GGT TCR GAG ACT TCC TGC CTA GGC CTC ATC CTC CTC 48  
Met Val Ser Asn Ala Ser Glu Thr Ser Cys Leu Gly Leu Ile Leu Leu  
-20 -15 -10

TTT GCC AGT CAC CTG ATT AAC CAA TTC TCC AGC 81  
Phe Ala Ser His Leu Ile Asn Gln Phe Ser Ser  
-5 1

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..302
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..274  
id H18735  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..302
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 116..275  
id T80360  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 51..115  
id T80360  
est

(ix) FEATURE:

- (A) NAME/KEY: other



(B) LOCATION: 29..69  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..41  
id T30360  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 66..302  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..237  
id AA137006  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 301..336  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 412..447  
id AA137006  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 65..302  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 2..239  
id HSC2CA081  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 64..224  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..161  
id T36290  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 223..302  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 161..240  
id T36290  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 2..220  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6  
seq LIVFISVCTALLA/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

```

A ATG CCC CGG AAG CGG AAG TGC GAT CTT CGG GCT GTC AGA GTT GGT CTG 49
 Met Pro Arg Lys Arg Lys Cys Asp Leu Arg Ala Val Arg Val Gly Leu
 -70 -65 -60

TTA CTC GGT GGT GGC GGA GTC TAC GGA AGC CGT TTT CGC TTC ACT TTT 97
Leu Leu Gly Gly Gly Gly Val Tyr Gly Ser Arg Phe Arg Phe Thr Phe
 -55 -50 -45

CCT GGC TGT AGA GCG CTT TCC CCC TGG CGG GTG AGA VTG CAG AGA CGA 145
Pro Gly Cys Arg Ala Leu Ser Pro Trp Arg Val Arg Xaa Gln Arg Arg
 -40 -35 -30

AGC TGC GAG ATG AGC ACT ATG TTC GCG GAC ACT CTC CTC ATC GTT TTT 193
Arg Cys Glu Met Ser Thr Met Phe Ala Asp Thr Leu Leu Ile Val Phe
 -25 -20 -15 -10

ATC TCT GTG TGC ACG GCT CTG CTC GCA GAG GGC ATA ACC TGG STC CTG 241
Ile Ser Val Cys Thr Ala Leu Leu Ala Glu Gly Ile Thr Trp Val Leu
 -5 1 5

GTT TAC AGG ACA GAC AAG TAC AAG AGA CTG AAG GCA GAA GTG GAA AAA 289
Val Tyr Arg Thr Asp Lys Tyr Lys Arg Leu Lys Ala Glu Val Glu Lys
 10 15 20

CAG AGT AAA AAA TAT TTG ATG GTA GAG TGG TGG CAA ASC TTC CTT TTT 337
Gln Ser Lys Lys Tyr Leu Met Val Glu Trp Trp Gln Xaa Phe Leu Phe
 25 30 35

TAC CCC TCT TTC TTA SAT CCA AAG RCT GTC TCA TCG 373
Tyr Pro Ser Phe Leu Xaa Pro Lys Xaa Val Ser Ser
 40 45 50

```

## (2) INFORMATION FOR SEQ ID NO: 243:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 159..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 121..269  
id W31320  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..121

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..85  
id W31320  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 320..380  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 282..342  
id W31320  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 114..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 77..128  
id W31320  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 400..443  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 364..407  
id W31320  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 154..307  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 2..155  
id T27259  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 320..443  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 168..291  
id T27259  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 192..307  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 108..223  
id AA157646  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 64..95  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..32  
id AA157646  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 320..443  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 123..246  
id AA182962  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 198..307  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..110  
id AA182962  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 243..307  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 189..253  
id T71690  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 181..235  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 125..179  
id T71690  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 114..164  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 58..108  
id T71690  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 130..198  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.9  
seq LGAAALALLLANT/DV

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

```

CCCCGCCCT GGGACCCCTCC GGGCCGGGCG GTTTGGCCCC TTAGCGCCCG GCGTCGGGG 60
CGGTAAAAGG CCGGCAGAAG GGAGGCACTT GAGAAATGTC TTCTCTCCAG GACCCAAGTT 120
TTCTTCACC ATG GGG ATG TGG TCC ATT GGT GCA GGA GCC CTG GGG GCT GCT 171
 Met Gly Met Trp Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala
 -20 -15 -10

GCC TTG GCA TTG CTG CTT GCC AAC ACA GAC GTG TTT CTG TCC AAG CCC 219
Ala Leu Ala Leu Leu Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro
 -5 1 5

CAG AAA GCG GCC CTG GAG TAC CTG GAG GAT ATA GAC CTG AAA ACA CTG 267
Gln Lys Ala Ala Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu
 10 15 20

GAG AAG GAA CCA AGG ACT TTC AAA GCA AAG GAG CTA TGG GAA AAA AAT 315
Glu Lys Glu Pro Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn
 25 30 35

GGA GCT GTG ATT ATG GCC GTG CGG AGG CCA GGC TGT TTC CTC TST CGA 363
Gly Ala Val Ile Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg
 40 45 50 55

GAG GAA GCT GCG GAT CTG TCC TCC CTG AAA AGC ATG TTG GAC CAG CTG 411
Glu Glu Ala Ala Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu
 60 65 70

GGC GTC CCC CTC TAT GCA GTG GTA AAG GAG CAA CGG 447
Gly Val Pro Leu Tyr Ala Val Val Lys Glu Gln Arg
 75 80

```

## (2) INFORMATION FOR SEQ ID NO: 244:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 13..394  
id C17481  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 379..424  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 390..435  
id C17481  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 66..256  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 72..262  
id T46941  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 1..67  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 6..72  
id T46941  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(149..271)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 1..123  
id R75331  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 257..430  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 42..215  
id W95977  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 278..430  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 5..157  
id R57521  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 255..347  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.9  
seq LPLLLVANAGTAA/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

```

ATGAAAATGG GTGTGCTTAT TTCCACGAAAG AGGAAAGAGA AGGACTTGCA AAGATATGTA 60
GGCTTGCCAT TCATTCTCGA TAAGAAGACT TCGTAGTGGA TGGCTTCAAT GTGTTATATA 120
ACAAGAAGCC TGTCATATAT CTTAGTGCTG CTGCTAGACC TGGCCTGGGC CAATACCTTT 180
GTAATCAGCT CGGCTTGCCC TTCCCCTGCT TGTGCCGTGT ACCCTGTAAC ACTGTGTTTG 240
GATCCCAGCA TCAG ATG GAT GTT GCC TTC CTG GAG ADA CTG ATT AAA GAT 290
 Met Asp Val Ala Phe Leu Glu Xaa Leu Ile Lys Asp
 -30 -25 -20
GAT ATA GAG CGA GGA AGA CTG CCC CTG TTG CTT GTC GCA AAT GCA GGA 338
Asp Ile Glu Arg Gly Arg Leu Pro Leu Leu Val Ala Asn Ala Gly
 -15 -10 -5
ACG GCA GCA GTA GGA CAC ACA GAC AAG ATT GGG AGA TTG AAA GAA CTC 386
Thr Ala Ala Val Gly His Thr Asp Lys Ile Gly Arg Leu Lys Glu Leu
 1 5 10
TGT GAG CAG TAT GGC ATA TGG CTT CAT GTG GAG GGT GTG AAT 428
Cys Glu Gln Tyr Gly Ile Trp Leu His Val Glu Gly Val Asn
 15 20 25

```

## (2) INFORMATION FOR SEQ ID NO: 245:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 3..232  
id HSC1WH101  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 41..169  
id R12437  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 63..104  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..42  
id R12437  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 63..230  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..168  
id R13448  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 165..212  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 36..83  
id T69236  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 180..227  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.8  
seq LFNLLWLALACSP/VW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

|                                                                 |            |            |            |            |            |     |
|-----------------------------------------------------------------|------------|------------|------------|------------|------------|-----|
| GTITGTGGCC                                                      | GTCCGGCCTC | CCTGACATGC | AGATTTCAC  | CCAGAAGACA | GAGAAGGAGC | 60  |
| CAGTGGTCAT                                                      | GGAATGGGCT | GGGGTCAAAG | ACTGGGTGCC | TGGGAGCTGA | GGCAGCCACC | 120 |
| GTITCAGCCT                                                      | GGCCAGCCCT | CTGGACCCCG | AGGTTGGACC | CTACTGTGAC | ACACCTACC  | 179 |
| ATG CGG ACA CTC TTC AAC CTC CTC TGG CTT GCC CTG GCC TGC AGC CCT | 227        |            |            |            |            |     |
| Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro |            |            |            |            |            |     |
| -15 -10 -5                                                      |            |            |            |            |            |     |
| GTT TGG                                                         | 233        |            |            |            |            |     |
| Val Trp                                                         |            |            |            |            |            |     |
| 1                                                               |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA



## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 178..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 118..271  
id R60406  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 178..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 57..195  
id N78477  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 214..312
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq FICLQWALPHSEA/GD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```

AAAGGCAGGA CTGACGCAGA ATGACAACGG CAACACGACA AGAAGTCCTT GGCCTCTACC 60
GCAGCATTTT CAGGCTTGCG AGGAAATGGC AGGCGACATC AGGGCAGATG GAAGACACCA 120
TCAAAGAAAA ACAGTACATA CTAAATGAAG CCAGAACGCT GTTCCGGAAA AACAAAAATC 180
TCACGGACAC AGACCTAATT AAACAGTGTA TAG ATG AAT GCA CAG CCA GGA TTG 234
 Met Asn Ala Gln Pro Gly Leu
 -30
-
AWA TTG GAC TGC ATT ACA AGA TTC CTT ACC CAN GGC CAA TTC ATC TGC 282
Xaa Leu Asp Cys Ile Thr Arg Phe Leu Thr Xaa Gly Gln Phe Ile Cys
-25 -20 -15
CTC CAA TGG GCC TTA CCC CAC TCC GAG GCC GGG GAC TTC GAA GCC AAG 330
Leu Gln Trp Ala Leu Pro His Ser Glu Ala Gly Asp Phe Glu Ala Lys
-10 -5 1 5

```

## (2) INFORMATION FOR SEQ ID NO: 247:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(230..352)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 32..154  
id W60134  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(78..189)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 195..306  
id W60134  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(9..87)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 298..376  
id W60134  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(176..352)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 57..233  
id H64097  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(57..189)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 219..351  
id H64097  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(34..352)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 57..325  
id W00624  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(1..70)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 337..406  
id W00624  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(1..168)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 156..323  
id W67127  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(167..323)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 2..158  
id W67127  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(64..352)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 58..346  
id H10776  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(23..64)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 347..388  
id H10776  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 120..326  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.7  
seq LCRLCLVRLFC/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

```
ATTGCGGAG GGSCACTGTC TCTTTTCTCT CTCATTTTAA AATGAAGTG TTGTTGCCTT 60
TGTATGTGGT TCAACCATCC AGCTCCACG TGGCTAAACT TTGCTCCAG TGGTCAAAG 119
ATG GCA AAA GAG TGG GGT TGG CAG GAG ATG GAA AAC GGA GGT GCC GCC 167
Met Gly Lys Glu Trp Gly Trp Gln Glu Met Glu Asn Gly Gly Ala Ala
 -65 -60 -55
```

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CCA GCA TGG GGG GCA GGT GGG GCA GTC CAC CCT GCC CCT CCC CCT GTG | 215 |
| Pro Ala Trp Gly Ala Gly Pro Pro Val His Pro Ala Pro Pro Pro Val |     |
| -50 -45 -40                                                     |     |
|                                                                 |     |
| GAG AAG ACG CTT AGT TGG GGG TGT GGG TTT GGG CTC CAT TCT GGA TTC | 263 |
| Glu Lys Thr Leu Ser Trp Gly Cys Gly Phe Gly Leu His Ser Gly Phe |     |
| -35 -30 -25                                                     |     |
|                                                                 |     |
| GGC GGT TCC GGG GGA GGG CTC GGT CTG TGC CGA TTA CTC TGT CTT GTA | 311 |
| Gly Gly Ser Gly Gly Gly Val Gly Leu Cys Arg Leu Leu Cys Leu Val |     |
| -20 -15 -10                                                     |     |
|                                                                 |     |
| CGT TTG TTC TGC TGC TCT TCA ATA TTG TAT CAA CGC CAG AAG         | 353 |
| Arg Leu Phe Cys Cys Ser Ser Ile Leu Tyr Gln Arg Gln Lys         |     |
| -5 1 5                                                          |     |

## (2) INFORMATION FOR SEQ ID NO: 248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..71
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..50  
id R82719  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..62
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 1..44  
id AA069083  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..52
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 2..34  
id R29193  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 23..52  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 10..39  
id AA158081  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 10..96  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.7  
seq AALLLTATVRLSA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

```
AAGTCCAAC ATG GCG GCG CCC AGC GGA GGG TGG AAC GGC GTC GGC GCG AGC 51
 Met Ala Ala Pro Ser Gly Gly Trp Asn Gly Val Gly Ala Ser
 -25 -20

TTG TGG GCG GCG CTG CTC CTC ACT GCC ACA GTC AGA CTT TCA GGT TGT 99
Leu Trp Ala Ala Leu Leu Thr Ala Thr Val Arg Leu Ser Ala Ser
-15 -10 -5 1

CCC GGC CCA 108
Pro Gly Pro
```

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 7..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..159  
id R24141  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 178..264  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 173..259  
id R24141  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 258..299  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 254..295  
                           id R24141  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 230..349  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 1..120  
                           id H25030  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 4..147  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.7  
                           seq LLLFFGKLLVVGG/VG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATC ATG ATC GCC ATC TAC GGG AAG AAT TTC TGT GTC TCA GCC AAA AAT | 48  |
| Met Ile Ala Ile Tyr Gly Lys Asn Phe Cys Val Ser Ala Lys Asn     |     |
| -45 -40 -35                                                     |     |
| GCG TTC ATG CTA CTC ATG CGA AAC ATT GTC AGG GTG GTC GTC CTG GAC | 96  |
| Ala Phe Met Leu Leu Met Arg Asn Ile Val Arg Val Val Val Leu Asp |     |
| -30 -25 -20                                                     |     |
| AAA GTC ACA GAC CTG CTG CTG TTC TTT GGG AAG CTG CTG GTG GTC GGA | 144 |
| Lys Val Thr Asp Leu Leu Leu Phe Phe Gly Lys Leu Leu Val Val Gly |     |
| -15 -10 -5                                                      |     |
| GGC GTG GGG GTC CTG TCC TTC TTT TTT TTC TCC GGT CGC ATC CCG GGG | 192 |
| Gly Val Gly Val Leu Ser Phe Phe Phe Phe Ser Gly Arg Ile Pro Gly |     |
| 1 5 10 15                                                       |     |
| CTG GGT AAA GAC TTT AAG AGC CCC CAC CTC AAC TAT TAC TGG CTG CCC | 240 |
| Leu Gly Lys Asp Phe Lys Ser Pro His Leu Asn Tyr Tyr Trp Leu Pro |     |
| 20 25 30                                                        |     |
| AYC ATG ACC TCC ATC CTG GGG GCC TAT GTC ATC GCC AGY GGC TTC TTC | 288 |
| Xaa Met Thr Ser Ile Leu Gly Ala Tyr Val Ile Ala Ser Gly Phe Phe |     |
| 35 40 45                                                        |     |
| AGC GTT TTC GGC ATG TGT GTG GAC ACG CTC TTC CTC TGC TTC CTG GAA | 336 |
| Ser Val Phe Gly Met Cys Val Asp Thr Leu Phe Leu Cys Phe Leu Glu |     |
| 50 55 60                                                        |     |
| GAC CTG GAG CGG ACA ACG GCT CCC TGG ACG GCC CTA CTA CAT GTC CAA | 384 |
| Asp Leu Glu Arg Thr Thr Ala Pro Trp Thr Ala Leu Leu His Val Gln |     |
| 65 70 75                                                        |     |

GAG CTT CTA  
Glu Leu Leu  
80

393

## (2) INFORMATION FOR SEQ ID NO: 250:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 222..265
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 220..263  
id N89186  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 76..348
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq SVLELIVASVCQS/HI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

```

GCTACTTTCT TTTTCAGTCT TTCGGTGCGG AGAAGGGGAG GAGGCGGGCA GAGGTCTGAA 60
AAAATCGAAT GCCTT ATG GAA AGG AAC TGC AAG GGT TCC TTT GGG GTG ATC 111
 Met Glu Arg Asn Cys Lys Gly Ser Phe Gly Val Ile
 -90 -85 -80

AAA GAG GGA GAC ACA GAC ACA GRR GAG ACA AAG GCA AGG AGG ACT GTC 159
Lys Glu Gly Asp Thr Asp Thr Xaa Glu Thr Lys Ala Arg Arg Thr Val
 -75 -70 -65

TGG GAG CCA CGC GGG CGA TAC AGT TTC CGA GRM ACG CCG CGT CCC GCC 207
Trp Glu Pro Arg Gly Arg Tyr Ser Phe Arg Xaa Thr Pro Arg Pro Ala
 -60 -55 -50

TAT CCI GTT GAA CAG TGC GGA TTT GCG AGG CGC GCC CTG GAG CTG CTA 255
Tyr Pro Val Glu Gln Cys Gly Phe Ala Arg Arg Ala Leu Glu Leu Leu
 -45 -40 -35

GAG ATC CGG AAG CAC AGC CCC GAG GTG TGC GAA CCA CCA AAC ATC CCA 303
Glu Ile Arg Lys His Ser Pro Glu Val Cys Glu Pro Pro Asn Ile Pro
 -30 -25 -20

```

GTT ACC AGT GTC CTT GAA TTG ATA GTG GGT TCT GTT TGT CAG TCT CAT 351  
 Val Thr Ser Val Leu Glu Leu Ile Val Ala Ser Val Cys Gln Ser His  
 -15 -10 -5 1

ATA AGA ACT ACT 363  
 Ile Arg Thr Thr  
 5

## (2) INFORMATION FOR SEQ ID NO: 251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
 region 1..243  
 id AA211459  
 est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 15..212
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
 seq LYMLAEALPVSHG/AH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

GTGAAGATGA AGCC ATG TTT GTA GAA TAT AGA AAA CAA CTG AAG TTA CTG 50  
 Met Phe Val Glu Tyr Arg Lys Gln Leu Lys Leu Leu  
 -65 -60 -55

TTG GAC AGG CTT GCT CAA GTT TCA CCA GAG TTA CTA CTG GCC TCT GTT 98  
 Leu Asp Arg Leu Ala Gln Val Ser Pro Glu Leu Leu Leu Ala Ser Val  
 -50 -45 -40

CGC AGA GTT TTT AGT TCT ACA CTG CAG AAT TGG CAG ACT ACA CGG TTT 146  
 Arg Arg Val Phe Ser Ser Thr Leu Gln Asn Trp Gln Thr Thr Arg Phe  
 -35 -30 -25

ATG GAA GTT GAA GTA GCA ATA AGA TTG CTG TAT ATG TTG GCA GAA GCT 194  
 Met Glu Val Glu Val Ala Ile Arg Leu Leu Tyr Met Leu Ala Glu Ala  
 -20 -15 -10

CIT CCA GTA TCT CAT GST GCT CAC TTC TCA GGT GAT GTT TCA AAA GCT 242  
 Leu Pro Val Ser His Gly Ala His Phe Ser Gly Asp Val Ser Lys Ala



|                                                                 | 1  | 5  | 10 |     |
|-----------------------------------------------------------------|----|----|----|-----|
| AST GCT TTG CAG GAT ATG ATG CGA ACT CTG GTA ACA TCA GGA GTC AGC |    |    |    | 290 |
| Ser Ala Leu Gln Asp Met Met Arg Thr Leu Val Thr Ser Gly Val Ser |    |    |    |     |
|                                                                 | 15 | 20 | 25 |     |
| GGG                                                             |    |    |    | 293 |
| Gly                                                             |    |    |    |     |

## (2) INFORMATION FOR SEQ ID NO: 252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 155..187
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 95..127  
id H83489  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 326..388
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq IIFLIQWHG3VFQ/EF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| AAGTCCCTGT ACAGGGTTTC TGACCTGTGG TAAAAACAGA ATGTCACCTTT CTGACAGGCA | 60  |
| CAGTACCCCC AGGATAAACT TGGAACCTCG AGAGGAAATT CACGAAACTC GTGGGGGCAG  | 120 |
| GGGTCACAAG GTGCTTGGTG GGGGARAASC TGGAAGACAT ATTGTCCAGG AGAAGGAATG  | 180 |
| TCACAAGGAA CTGACAAAAT CAAGTCACGG CGCCTACAAA GATGAGGGGC AGATTCTGGC  | 240 |
| TGCCTTTTAA TTTCGTCTTT CACCTGATAT CTGTGCCAGA GAATGATAAA AATCATAATA  | 300 |
| AAGGRAATAG YGGAAGAGGA GACTT ATG TTA CTG GGG ACA TCT AAC ATA ATT    | 352 |
|                                                                    |     |
| Met Leu Leu Gly Thr Ser Asn Ile Ile                                |     |
| -20 -15                                                            |     |
| ATT TTC CTG ATT CAG TGG CAT GGT TCA GTC TTC CAG GAG TTC            | 394 |
| Ile Phe Leu Ile Gln Trp His Gly Ser Val Phe Gln Glu Phe            |     |
| -10 -5 1                                                           |     |

## (2) INFORMATION FOR SEQ ID NO: 253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 48..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 35..225  
id HSC0CC021  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..49
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..35  
id HSC0CC021  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..212  
id T32119  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 36..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..203  
id T35494  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 13..202  
id HUMHG5097  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 51..238  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 1..188  
 id AA027882  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 78..137  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.6  
 seq AFVXACVLSLIST/IY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

```

AAGAGTAGGG TGCTGTGGTC TGAGCTAGAG GGTGAAGCTG GCGGASAGGA GGATGGGCGA 60
GCAGTCTGAA TGCCAGA ATG GRT AAC CGT TTT GCT ACA GCA TTT GTA ATD 110
 Met Xaa Asn Arg Phe Ala Thr Ala Phe Val Xaa
 -20 -15 -10
GCT TGT GTG CTT AGC CTC ATT TCC ACC ATC TAC ATG GCA GCC TCC ATT 158
Ala Cys Val Leu Ser Leu Ile Ser Thr Ile Tyr Met Ala Ala Ser Ile
 -5 1 5
GGC ACA GAC TTC TGG TAT GAA TAT CGA AGT CCA GTT CAA GAA AAT TCC 206
Gly Thr Asp Phe Trp Tyr Glu Tyr Arg Ser Pro Val Gln Glu Asn Ser
 10 15 20
AGT GAT TTG AAT AAA AGC ATC TGG GAT GAA TTG 239
Ser Asp Leu Asn Lys Ser Ile Trp Asp Glu Leu
 25 30

```

## (2) INFORMATION FOR SEQ ID NO: 254:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(43..130)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 176..263  
 id C01485

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(137..219)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 88..170  
id C01485  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 421..459
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq MSLTSGFLRVSG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

```

CACCAATGTT ATGAATGGCG TGGCCTCCTA CTGCCGTCCC TGTGCCCTAG AAGCCTCTGA 60
TGTGGGCTCC TCCTGCACCT CTTGTCCTGC TGTTACTAT ATTGACCGAG ATTCAGGAAC 120
CTGCCAMTCC BTGCCCCCCT AACACAATTC TGAAAGCCCA CCAGCCTTAT GGTGTCCAGG 180
CCTGTGTGCC CTGTGGTCCA GGGACCAAGA ACAACAAGAT CCACTCTCTG TGCTACAATG 240
ATTGCACCTT CTCACGCAAC ACTCCAACCA GGACTTTCAA CTACAACTTC TCCGCTTTGG 300
CAAACACCGT CACTCTTGCT GGAGGGCCAA GCTTCACTTC CAAAGGGTTG AAATACTTCC 360
ATCACTTTAC CCTCAGTCTC TGTGGAAACC AGGGTAGGAA AATGTCTGTG TGCACCGACA 420
ATG TCA CTG ACC TCC GGA TTC CTG AGG GTG AGT CAG GGT TCT CCA AAT 468
Met Ser Leu Thr Ser Gly Phe Leu Arg Val Ser Gln Gly Ser Pro Asn
 -10 -5 1

CTA TCA CAG 477
Leu Ser Gln
5 -

```

## (2) INFORMATION FOR SEQ ID NO: 255:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 55..316  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
 region 1..262  
 id H37671  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 102..261  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 50..209  
 id N47067  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 55..104  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 2..51  
 id N47067  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 251..316  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 14..79  
 id AA135001  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 58..246  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.6  
 seq AIRTLFSVTGILA/EQ

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AACTTGGCGC GCGGCSSGGC TGCAGACGGC TGCGAGGCGC TGGGCACAGG TGTCTG   | 57  |
| ATG GCA AAT TTC AAG GGC CAC GCG CTT CCA GGG AGT TTC TTC CTG ATC | 105 |
| Met Ala Asn Phe Lys Gly His Ala Leu Pro Gly Ser Phe Phe Leu Ile |     |
| -60 -55 -50                                                     |     |
| ATT GGG CTG TGT TGG TCA GTG AAG TAC CCG CTG AAG TAC TTT AGC CAC | 153 |
| Ile Gly Leu Cys Trp Ser Val Lys Tyr Pro Leu Lys Tyr Phe Ser His |     |
| -45 -40 -35                                                     |     |
| ACG CGG AAG AAC AGC CCA CTA CAT TAC TAT CAG CGT CTC GAG ATC GTC | 201 |
| Thr Arg Lys Asn Ser Pro Leu His Tyr Tyr Gln Arg Leu Glu Ile Val |     |
| -30 -25 -20                                                     |     |
| GAA GCC GCA ATT AGG ACT TTG TTT TCC GTC ACT GGG ATC CTG GCA GAG | 249 |
| Glu Ala Ala Ile Arg Thr Leu Phe Ser Val Thr Gly Ile Leu Ala Glu |     |
| -15 -10 -5 1                                                    |     |

CAG TTT GTT CCG GAT GGG CCC CAC CTG CAC CTC TAC CAT GAG AAC CAC 29  
Gln Phe Val Pro Asp Gly Pro His Leu His Leu Tyr His Glu Asn His  
5 10 15  
TGG ATA AAG TTA ATG AAT 315  
Trp Ile Lys Leu Met Asn  
20

## (2) INFORMATION FOR SEQ ID NO: 256:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 84..400  
id N34255  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..84  
id N34255  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..304
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 83..298  
id H79944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..54
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 2..48  
id H79944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 336..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 332..378  
id H79944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 304..340
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 299..335  
id H79944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..83
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 49..83  
id H79944  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 109..298
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 106..295  
id H73369  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 1..87  
id H73369  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 336..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 336..382  
id H73369  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 295..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 293..324  
id H73369

est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 164..237  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 142..215  
id AA132425  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 327..395  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 307..375  
id AA132425  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..88  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 3..70  
id AA132425  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 124..163  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 103..142  
id AA132425  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 109..298  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 24..213  
id R97376  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 296..405  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 212..321  
id R97376  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 187..342  
(C) IDENTIFICATION METHOD: Von Neijne matrix  
(D) OTHER INFORMATION: score 5.5



seq AGLLEKSLAGLGA/YQ

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

```

AGCAGGCACA ACAGAGCCGC TCCCWCTCC TCGCCCCGCC ACCGGGACGG AGAGCGCCCG 60
CGCCTGCATT TCGGGCGACA CCTCGCAGGT CATTCCTGCG GCTTGGCGCG CTTGTAGAC 120
AGCGGGGGCC TTCGTSAGAC CGGTGCAGGC CTGGGGTAST CTCTGTCTG GACAGAGAAG 180
AGAAAA ATG CAG GAC ACT GGC TCA GTA GTG GAT TTG CAT TGG TTT GGC 228
 Met Gln Asp Thr Gly Ser Val Val Pro Leu His Trp Phe Gly
 -50 -45 -40
TTT GGC TAC GCA GCA CTG GTT GCT TCT GGT GGG ATC ATT GGC TAT GTA 276
Phe Gly Tyr Ala Ala Leu Val Ala Ser Gly Gly Ile Ile Gly Tyr Val
 -35 -30 -25
AAA GCA GGC AGC GTG CCG TCC CTG GCT GCA GGG CTG CTC TTT GGC AGT 324
Lys Ala Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser
 -20 -15 -10
CTA GCC GGC CTG GGT GCT TAC CAG CTG TCT CAG GAT CCA AGG AAC GTT 372
Leu Ala Gly Leu Gly Ala Tyr Gln Leu Ser Gln Asp Pro Arg Asn Val
 -5 1 5 10
TGG GTT TTC CTA GCT ACA TCT GGT ACC TTG GCT 405
Trp Val Phe Leu Ala Thr Ser Gly Thr Leu Ala
 15 20

```

(2) INFORMATION FOR SEQ ID NO: 257:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 119..237
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 116..234  
id HSC2TH021  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 24..94  
id HSC2TH021  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 238..289  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 234..285  
id HSC2TH021  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 280..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 277..316  
id HSC2TH021  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 130..237  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 23..130  
id R59681  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 238..289  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 130..181  
id R59681  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 280..325  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 173..218  
id R59681  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 183..287  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.4  
seq CCALLTSLXCIWG/PA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

ACCTTCTGTI ACTGTCCGGG GCTGCGGGG TTGCTTCKG CGTCAWGGCT CAAAGGGCCT 60

```

TCCCGMATCC TTATGCTGAT TATAAGAAAT CCCTGDRCCG AAGSTACTTT GATGCTGCCG 120
GGARGCTGAC TCCTGASTTC TCACAACGCT TGACCAATAA GATTCGGGAG CTTCTTCAGC 180
AA ATG GAG AKA GGC CTG AAA TCA GCA GAC CCT CGG GAT GGC ACC GGT 227
 Met Glu Xaa Gly Leu Lys Ser Ala Asp Pro Arg Asp Gly Thr Gly
 -35 -30 -25
TAC ACT GRC TTN NKC ARG TAT TSC TGT GCT TTA CTT ACA TCT TTA TGR 275
 Tyr Thr Xaa Xaa Xaa Xaa Tyr Cys Cys Ala Leu Leu Thr Ser Leu Xaa
 -20 -15 -10 -5
TGT ATT TGG GGA CCT CCC TAC CTA CAG TTA GCA CAT GGC TAT GTA AAG 323
 Cys Ile Trp Gly Pro Ala Tyr Leu Gln Leu Ala His Gly Tyr Val Lys
 1 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 258:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 12..252  
id H64050  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..241  
id R17172  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 2..242  
id HSC15C081  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 8..241  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..234  
id AA149663  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 29..241  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 29..241  
id HSJ46380  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 10..135  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.4  
seq ITGVILLAVGIWG/KV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

```
GGGCTAGTC ATG GCG TCC CCG TCT CGG AGA CTG CAG ACT AAA CCA GTC ATT 51
 Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile
 -40 -35 -30

ACT TGT TTC AAG AGC GTT CTG CTA ATC TAC ACT TTT ATT TTC TGG ATC 99
 Thr Cys Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile
 -25 -20 -15

ACT GGC GTT ATC CTT CTT GCA GTT GGC ATT TGG GGC AAG GTG AGC CTG 147
 Thr Gly Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu
 -10 -5 1

GAG AAT TAC TTT TCT CTT TTA AAT GAG AAG GCC ACC AAT GTC CCC TTC 195
 Glu Asn Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe
 5 10 15 20

GTG CTC ATT GCT ACT GGT ACC GTC ATT ATT CTT TTG GGC ACC TTG 240
 Val Leu Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Leu
 25 30 35
```

## (2) INFORMATION FOR SEQ ID NO: 259:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 385 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..349
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 6..347  
id AA075824  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 344..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 341..382  
id AA075824  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 2..346  
id R55598  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..315  
id HSC33B061  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 156..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 91..320  
id T65515  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..141
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 5..76  
id T65515  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..305
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 2..273

Id HSCZRF061  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 119..319
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq LSVSLLEPCAGAWS/LL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

```

AAAAGCGGAG MYAGGMNCGG TGAGGAGAGT CGAGGGAGGT GACGCGCGCT GCCGGGGCGA 60
GGTTGCGAGG GCGGGTGTG AAGAATGTGT GGGCGAACAT CCTGTCACCT ACCTAGAG 118
ATG TTC TCA CGA GAG CTT GCG CCT ACC AGG ATC GGC GGG GCC AGC AGC 166
Met Phe Ser Arg Glu Leu Ala Pro Thr Arg Ile Gly Gly Ala Ser Ser
 -65 -60 -55
GGC TCC CGG AGT GGA GGG ACC CTG ATA AGT ACT GCC CCT CTT ACA ACA 214
Gly Ser Arg Ser Gly Gly Thr Leu Ile Ser Thr Ala Pro Leu Thr Thr
 -50 -45 -40
AGA GTC CTC AAT CCA ACA GCC CAG TGC TTC TGT CTC GAC TGC ACT TTG 262
Arg Val Leu Asn Pro Thr Ala Gln Cys Phe Cys Leu Asp Cys Thr Leu
 -35 -30 -25 -20
AGA AGG ATG CAG ACT CAT CTG ACC GTA TCA TTG CTC CCA TGC GCT GGG 310
Arg Arg Met Gln Thr His Leu Ser Val Ser Leu Leu Pro Cys Ala Gly
 -15 -10 -5
GCT TGG TCC CTT CTT RGT TCA AAG AAA GTG ATC CTT CCA AGC TGC AGT 358
Ala Trp Ser Leu Leu Xaa Ser Lys Lys Val Ile Leu Pro Ser Cys Ser
 1 5 10
TCA ATA CTA MCA ACT GTC GTA GTG ATA 385
Ser Ile Leu Xaa Thr Val Val Val Ile
 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 260:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..123
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 13..104  
id R49759  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 132..194  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 106..168  
id R49759  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 225..311  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.1  
seq LLMLGVTLPSYW/RV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

```

ATTCTCTGA CCTGCCAGGA AGCAGAGAGA CCCACAGAGC AGGCAGGGAG GCAGAAAGTG 60
GAGACGGACC TGAGCCCGAG GAAGAGGCAG GCAGAGGCTG AGGCTGATTC CACCCCAGCC 120
TGCCTGGRAC AAACCTCCT TAGCCGCAGC CCCTTCCAST TCCCTAGGGG TTCTGCCCTT 180
CCCCCTCTCT GGGGCACCAG CCCCCAGGG TCCTGCATCC NACC ATG TCG ATG GCT 236
 Met Ser Met Ala

GTG GAA ACC TTT GGC TTC TTC ATG GCA ACT GTG GGG CTG CTG ATG CTG 284
Val Glu Thr Phe Gly Phe Phe Met Ala Thr Val Gly Leu Leu Met Leu
-25 -20 -15 -10

GGG GTG ACT CTG CCA AAC AGC TAC TGG CGA GTG TCC ACT GTG CAC GGG 332
Gly Val Thr Leu Pro Asn Ser Tyr Trp Arg Val Ser Thr Val His Gly
 -5 1 5

AAC GTC ATC AHC ACC AAC AHC ATC TTC GAG AAC CTC TGG TTT AGC AGT 380
Asn Val Ile Xaa Thr Asn Xaa Ile Phe Glu Asn Leu Trp Phe Ser Ser
 10 15 20

GCC GGG 386
Ala Gly
 25

```

## (2) INFORMATION FOR SEQ ID NO: 261:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 112..216  
id T86663  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..156
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 120..153  
id AA055880  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 55..114
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5  
seq XFLXLXXLSXXWP/XD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```

ACTCAGAAGC TTGGACCGCA TCCTAGCCGC CGACTCACAC AAGGCAGABT TGCC ATG 57
 Met
 -20

GAG AAA ATT CCA GTG TCA SCA TTC TTG CDC CTN GYG GSC CTC TCK WAS 105
Glu Lys Ile Pro Val Ser Xaa Phe Leu Xaa Leu Xaa Xaa Leu Ser Xaa
 -15 -10 -5

AKC TGG CCA SSG GAT ACC ACA GTC AAA CCT GGA GCC AMA AAG GAC ACA 153
Xaa Trp Pro Xaa Asp Thr Thr Val Lys Pro Gly Ala Xaa Lys Asp Thr
 1 5 10

AAG GAC TCT CGA SCC AAA CTG CCC CAG ACC CTC TCC AGA GGT TGG GGT 201
Lys Asp Ser Arg Xaa Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp Gly
 15 20 25

GAC CAA CTC ATC TGG ACA CGG 222
Asp Gln Leu Ile Trp Thr Arg
 30 35

```

## (2) INFORMATION FOR SEQ ID NO: 262:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 207..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 85..204  
id W69716  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 122..208
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..87  
id W69716  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 316..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 195..245  
id W69716  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 282..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 94..178  
id W73842  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 207..287
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 17..97  
id W73842  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 257..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 42..111  
id W58103  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 317..366  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
 region 101..150  
 id W58108  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 112..312  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5  
 seq LILERPLVPSAEA/SG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```

ATAAGGCCTC AGGSTCCTGT TTTCCTGGC CTCTTCTAGA GGGCCCGTGG AMCAGGTCGC 60
AGTGCGTGCT TATTTGAAAA CCAGSTGTGT GAGCCGAATG CCTGCCAGGC C ATG CAC 117
 Met His

TCA GCA GAG GAG CCC TTG TAN CTG GCT GCC CTG AGA GGA GCA AGA GGC 165
Ser Ala Glu Glu Pro Leu Xaa Leu Ala Ala Leu Arg Gly Ala Arg Gly
-65 -60 -55 -50

CAC CTC CCA TGT GGC TCT AGA CAC CAC GTG GGC TCA TTA GCC CCA GCG 213
His Leu Pro Cys Gly Ser Arg His His Val Gly Ser Leu Ala Pro Ala
-45 -40 -35

TCT GTG CCG GCT CCA GGT GCC TGC CTC TGG GTG TGT GAG TGG GAG ACT 261
Ser Val Pro Ala Pro Gly Ala Cys Leu Trp Val Cys Glu Trp Glu Thr
-30 -25 -20

TTG CTC CCT GGC CTC ATC CTA GAG AGG CCC CTG GTG CCT AGT GCT GAG 309
Leu Leu Pro Gly Leu Ile Leu Glu Arg Pro Leu Val Pro Ser Ala Glu
-15 -10 -5

GCC TCT GGG GCT GGA AAG CTC AGC AGA AAG GAG GCA CTA CTG AGC AAC 357
Ala Ser Gly Ala Gly Lys Leu Ser Arg Lys Glu Ala Leu Leu Ser Asn
 1 5 10 15

TAT GCA TTG 366
Tyr Ala Leu

```

## (2) INFORMATION FOR SEQ ID NO: 263:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 121..264  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 127..270  
id N24991  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 3..124  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 10..131  
id N24991  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 161..292  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 15..146  
id HSC1WG111  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 176..310  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..135  
id AA001396  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 176..265  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..90  
id AA017578  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 191..265  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..75  
id R17530  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 167..295  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.9

seq GLWLALVDGLVRX/AP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```

ACTTTTTCCT ACGCAGCCGC TCCTGCCGCC GTGGTCGCTG GAGCTTTGCC TCTCTAGGCC 60
GGCAGCGCCT CTCTCCATG GTCCTGTCTG TCAGCGCTGT TTTGAGAGCC CGCCGGTGAG 120
CCCGSGCCAC GCTCAGACAC TTCGATCGTC GAGTCTGTCA CTGGGG ATG GCG GGT 175
 Met Ala Gly
CAG TTC CGC AGC TAC GTG TGG GAC CCG CTG CTG ATC CTG TCG CAG ATC 223
Gln Phe Arg Ser Tyr Val Trp Asp Pro Leu Leu Ile Leu Ser Gln Ile
-40 -35 -30 -25
GTC CTC ATG CAG ACC GTG TAT TAC GGC TCG CTG GGC CTG TGG CTG GCG 271
Val Leu Met Gln Thr Val Tyr Tyr Gly Ser Leu Gly Leu Trp Leu Ala
 -20 -15 -10
CTG GTG GAC GGG CTA GTG CGA ASA GCC CCT CGC TGG ATC SCA GCG 316
Leu Val Asp Gly Leu Val Arg Xaa Ala Pro Arg Trp Ile Xaa Gly
 -5 1 5

```

(2) INFORMATION FOR SEQ ID NO: 264:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 72..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 76..316  
id W03477  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..78
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 7..83  
id W03477  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 72..328

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 69..325  
id W40364  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 3..78  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..76  
id W40364  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 164..328  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 172..336  
id R71313  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 72..158  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 80..166  
id R71313  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 7..78  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 16..87  
id R71313  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 164..328  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 151..315  
id H87810  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 72..158  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 59..145  
id H87810  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 14..78  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 2..66  
id H87810  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 72..274  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 52..254  
id AA135694  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 20..78  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..59  
id AA135694  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 270..328  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 249..307  
id AA135694  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 62..295  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.9  
seq VGAVFGLTTCISA/HV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

```
AGGCTGCCCT TCGCTTCCC GAGCTGGCGG GGTCCGTGGT GCGGGATCGA GATTGCGGGC 60
T ATG GCG CCG AAG GTT TTT CGI CAG TAC TGG GAT ATC CCC GAT GGC ACC 109
 Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr
 -75 -70 -65

GAT TGC CAC CGC AAA GCC TAC AGC ACC ACC AGT ATT GCC AGC GTC GCT 157
Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala
 -60 -55 -50

GGC CTG ACC GCC GCT GCC TAC AGA CTC ACA CTC AAT CCT CCG GGC ACC 205
Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr
 -45 -40 -35

TTC GTT GAA GGA GTG GCT AAG GTT GGA CAA TAC ACG TTC ACT GCA GCT 253
Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
```

-30                      -25                      -20                      -15

GCT GTC GGG GCC GTG TTT GGC CTC ACC ACC TGC ATC AGC GCC CAG GTC      301  
Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val  
                    -10                      -5                      1

CCC GAG AAG CCC GAC GAC CCC CTG AAC CGG                      331  
Arg Glu Lys Pro Asp Asp Pro Leu Asn Arg  
                    5                      10

## (2) INFORMATION FOR SEQ ID NO: 265:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(44..183)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..140  
id N78549  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..34)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 150..182  
id N78549  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(103..214)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 100..211  
id N27605  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 150..203
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq WLQVLPVILLLLG/VP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```

AGAGAGAGGG GCCGCTACGC CGCACAGCAA ACAAGCTCCG CGACGTTTCC AGGACCCGGA 60
TAATCCCGCC CTTAGAGCAG AGCCGGAAGA AGSCGGGACG AACCGGAAGA GGGTGAAATG 120
CITTCGGTAG GCACTCCACG GCTGTGAAG ATG GCG GCG GCT GCG TGG CTT CAG 173
 Met Ala Ala Ala Ala Trp Leu Gln
 -15

GTG TTG CCT GTC ATT CTT CTG CTT CTG GGA GTC CCC CCG TCS 215
Val Leu Pro Val Ile Leu Leu Leu Gly Val Pro Pro Ser
-10 -5 1

```

## (2) INFORMATION FOR SEQ ID NO: 266:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 59..182  
id AA045287  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 45..168  
id R77973  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 70..193  
id AAL36043  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..124)
- (C) IDENTIFICATION METHOD: blastn



(D) OTHER INFORMATION: identity 100  
region 60..183  
id AA115201  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(1..124)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 60..183  
id R72616  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 5..115  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.3  
seq LLILDMNVLYTDA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| ATAG ATG GAA ATA TAC TTT ATA TTT TGT ATC ATC GTG CCT ATA GCC GCT | 49  |
| Met Glu Ile Tyr Phe Ile Phe Cys Ile Ile Val Pro Ile Ala Ala      |     |
| -35 -30 -25                                                      |     |
| GCC ACC GTG TAT AAA TCC TGG TGT CTG CTC CTT ATC CTG GAC ATG AAT  | 97  |
| Ala Thr Val Tyr Lys Ser Trp Cys Leu Leu Leu Ile Leu Asp Met Asn  |     |
| -20 -15 -10                                                      |     |
| GTA TTG TAC ACT GAC GCG TCC CCA CTC GGG                          | 127 |
| Val Leu Tyr Thr Asp Ala Ser Pro Leu Gly                          |     |
| -5 1                                                             |     |

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 48..140  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 36..128  
id AA054941  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 130..197  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 117..184  
id AA054941  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 48..218  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 36..206  
id W68324  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 48..141  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 22..115  
id H72703  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 130..218  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 103..191  
id H72703  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 29..59  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 4..34  
id H72703  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 48..140  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 16..108  
id AA128297  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 130..218  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 97..135  
id AA128297

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 48..141  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                           region 13..106  
                           id W25240  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 130..218  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 94..182  
                           id W25240  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 71..163  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.8  
                           seq VLLAIGMFFTAWF/FV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```

ACTGTCGACG TGTTCTTCCG GTGGCGGACG GCGGATTAGC CTTCGCGGGG CAAAATTGRA 60
RCYCDRGGCC ATG AGC AGA TAT ACC AGC CCA GTG AAC CCA GCT GTC TTC 109
 Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala Val Phe
 -30 -25 -20

CCC CAT CTG ACC GTG GTG CTT TTG GCC ATT GGC ATG TTC TTC ACC GCC 157
Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr Ala
 -15 -10 -5

TGG TTC TTC GTT TAC GAG GTC ACC TCT ACC AAG TAC ACT CGT GAT ATC 205
Trp Phe Phe Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg Asp Ile
 1 5 10

TAT AAA GAG CTC CAG 220
Tyr Lys Glu Leu Gln
 15

```

## (2) INFORMATION FOR SEQ ID NO: 268:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 422 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 135..179  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 15..59  
id R68571  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 309..413  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.8  
seq LMLSSSLPLLIWL/KD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

```

AACTTTAGCC TCTGATTGCA GGCCACCACT TCATTACAT GGGGTGAGCA CCAATGCGTT 60
TTGTTCAATT CTTTGTTCAA AACCCCAAGA ATCTGGACAA CTGCACTCA AGACCCCTCA 120
CGGGTTTGGC GAGCCAGTCC TTCAGTGGCT GTTTTCTAGT AGCTCCTTGG CAATTGAGGG 180
GAACTGGCTG GGACCACTCT CCAGTGCTGT CTGAAGGCCA AGGAGTGAAC AGGGATGGCT 240
GCCCTGCCTT GAAGAGGGAA GGA CTCTTTT CTATCCTTTC CAGCTATAGT CCCTGATCCC 300
TACATGTG ATG CGG TTG GCA GCG GAA GCT CAT CCT GGG CGA ACT CAC ACA 350
Met Arg Leu Ala Ala Glu Ala His Pro Gly Arg Thr His Thr
-35 -30 -25

CTT TTC AGG AGA CTT AAA CCT TTT CTT ATG CTA AGT TCT TCC CTT CCC 398
Leu Phe Arg Arg Leu Lys Pro Phe Leu Met Leu Ser Ser Ser Leu Pro
-20 -15 -10

CTA CTC ATC TGG CTA AAG GAC AGA 422
Leu Leu Ile Trp Leu Lys Asp Arg
-5 1

```

## (2) INFORMATION FOR SEQ ID NO: 269:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 17..276  
id N23506  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..220  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 8..226  
id R74310  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 219..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 226..268  
id R74310  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 103..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 125..283  
id N42319  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 103..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 119..277  
id N33735  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 105..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 143..299  
id R23867  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 97..213  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.8  
seq IILFSAIVGFIYG/YV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```

AAATGCCRRR CCTAGCCCT CACGGTCCTT AAGTCTCGGT CGCCCTCGCC TCKAGCCTG 60
CCVBCCGCGC TCRKCTGSSC GACTCCTCAG SCAGCC ATG CTG GAG CAT CTG RGC 114
 Met Leu Glu His Leu Xaa
 -35

TCG CTG CCC ACC CAG ATG GAT TAC AAG GGC CAG AAG CTA CCT GRR CAG 162
Ser Leu Pro Thr Gln Met Asp Tyr Lys Gly Gln Lys Leu Ala Xaa Gln
-30 -25 -20

ATG TTT CAG GGR ATT ATT CTT TTT TCT GCA ATA GTT GGA TTT ATC TAC 210
Met Phe Gln Gly Ile Ile Leu Phe Ser Ala Ile Val Gly Phe Ile Tyr
-15 -10 -5

GGG TAC GTG GCT GAA CAG TTC GGG TGG ACT GTC TAT ATA GTT ATG GCC 258
Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr Val Tyr Ile Val Met Ala
1 5 10 15

GGA 261
Gly

```

## (2) INFORMATION FOR SEQ ID NO: 270:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(154..354)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 70..270  
id AA164185  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..111
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 298..381  
id AA164184  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 297..344
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.8  
seq SKVLEKSPUNVLG/ED

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

```

CCAACGTGTG CTTTGAAAAA AAGAAGGGAT GTTTTCTGTG TCAATGAAG STAATCATAG 60
ATCAAATTTG CTTATTGTCT TGTTCAAATC CTAGAAAACC ATTAGCATTT TTCTTTGCTT 120
GTAATATKAG AATCTAACAC TCATACAGAA TATTGGAAGG GTTACCCTAC AATTGTAAAT 180
TTGAAATTCT CCTTCTAATT CTGTCAGTTA TTTATTGACA TAGTAGTGGT TCTGTAGTCA 240
AGTGCATATA AGSTTTTGAA TGTTACATCT TATTNNNGGA TTWTTATTTT ATCATT ATG 299
 Met
GAG TAT AGC AAA GTT CTA TTT TGT TCT TTT TCA AAT GTA CTT GGT TTT 347
Glu Tyr Ser Lys Val Leu Phe Cys Ser Phe Ser Asn Val Leu Gly Phe
-15 -10 -5 1

GAT TAT 353
Asp Tyr

```

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..133
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..115  
id HSC13B041  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 105..207  
id HSC13B041  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..226

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 71..173  
id T08849  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 53..133  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..81  
id T08849  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 53..135  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..83  
id H88132  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 124..192  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 71..139  
id H88132  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 192..226  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 140..174  
id H88132  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 53..144  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..92  
id T33149  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 145..226  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 92..173  
id T33149  
est

(ix) FEATURE:



(A) NAME/KEY: other  
 (B) LOCATION: 52..133  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 1..82  
                           id AA121114  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 192..226  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 141..175  
                           id AA121114  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 46..123  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.7  
                           seq LIMQLGSVLLTRC/PF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```

ACTCTCTGAC TGGGGTGAGG CCGCAGCGGA CTGCCCTTTC CSAAG ATG GCG TCG AAG 57
 Met Ala Ser Lys
 -25

ATA GGT TCG AGA CGG TGG ATG TTG CAG CTG ATC ATG CAG TTG GGT TCG 105
Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met Gln Leu Gly Ser
 -20 -15 -10

GTG CTG CTC ACA CGC TGC CCC TTT TGG GGC TGC TTC AGC CAG CTC ATG 153
Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe Ser Gln Leu Met
 -5 1 5 10

CTG TAC GCT GAG AGG GCT GAG GCA CGC CGG AAG CCC GAC ATC CCA GTG 201
Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro Asp Ile Pro Val
 - 15 20 25

CCT TAC CTG TAT TTC GAC AGT GGG 225
Pro Tyr Leu Tyr Phe Asp Ser Gly
 30

```

## (2) INFORMATION FOR SEQ ID NO: 272:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..287  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 9..294  
id W52125  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..283  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..265  
id AA024623  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 22..284  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..263  
id H55824  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..307  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 2..288  
id R62921  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 102..287  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 57..242  
id N31702  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 45..100  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..56  
id N31702  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 69..224  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.7

seq LGLALGRLEGGSA/RH

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

```

ATTGGCTCCG GATCGTGCCT GAGGCGGCTT CGTGGGCAGC GAGAGTCACA GACAAGACAG 60
CAAGCAGG ATG GAG CAC TAC CGG AAA GCT GGC TCT GTA GAG CTC CCA GCG 110
 Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala
 -50 -45 -40

CCT TCC CCA ATG CCC CAG CTA CCT CCT GAT ACC CTT GAG ATG CGG GTC 158
Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val
 -35 -30 -25

CGA GAT GGC AGC AAA ATT CGC AAC CTG CTG GGG TTG GCT CTG GGT CGG 206
Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg
 -20 -15 -10

TTG GAG GGC GGC AGT GCT CGG CAT GTA GTG TTC TCA GGT TCT GGC AGG 254
Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg
 -5 1 5 10

GCT GCA GGA AAG GCT GTC AGC TGC GCT GAG ATT GTC AAG CGG CGG GTC 302
Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val
 15 20 25

CCG 305
Pro

```

(2) INFORMATION FOR SEQ ID NO: 273:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 2..213  
id W26501  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 6..219

id W28013  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(211..324)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 334..447  
id W28077  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 215..324  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..110  
id HSC3LG011  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 104..181  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.6  
seq LIALTCLDGTTVS/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

```

AGCATTTTGC AAAGATGGCT GTAGGAATGG AGGAGCCTGT ATTGCCGCTA ATGTGTGTGC 60
CTGCCCCACAA GGCTTCACTG GACCCAGCTG TGAAACGACA TTG ATG AAT GCT CTG 115
 Met Asn Ala Leu
 -25
ATG GTT TTG TTC AAT GTG ACA GTC GTG CTA ATT GCA TTA ACC TGC CTG 163
Met Val Leu Phe Asn Val Thr Val Val Leu Ile Ala Leu Thr Cys Leu
-20 -15 -10
GAT GGT ACC ACT GTG AGT GCA GAG ATG GCT ACC ATG ACA ATG GGA TGT 211
Asp Gly Thr Thr Val Ser Ala Glu Met Ala Thr Met Thr Met Gly Cys
-5 1 5 10
TTT CAC CAA GTG GAG AAT CGT GTG AAG ATA TTG ATG AGT GTG GCA CCG 259
Phe His Gln Val Glu Asn Arg Val Lys Ile Leu Met Ser Val Gly Pro
15 20 25
GGA GGC ACA GCT GTG CCA ATG ATA CCA TTT GCT TCA ATT TGG ATG GCG 307
Gly Gly Thr Ala Val Pro Met Ile Pro Phe Ala Ser Ile Trp Met Ala
30 35 40
GAT ATG ATT GNC GAT 322
Asp Met Ile Xaa Asp
45

```

## (2) INFORMATION FOR SEQ ID NO: 274:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 32..97  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..66  
id AAL33635  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 191..325  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.6  
seq VLVYLVTAEKRWVS/DD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

|                                                                 |                                                     |            |            |            |            |     |
|-----------------------------------------------------------------|-----------------------------------------------------|------------|------------|------------|------------|-----|
| ACTCCCAGGC                                                      | TGGGCCAGCA                                          | CACCCGGCAG | GCTCTGTCCT | GGAAACAGGC | TTCAACGGGC | 60  |
| TTCCCCGAAA                                                      | ACCTTCCCCG                                          | CTTCTGGRTA | TGAAVWTKCA | AGCTGCTTGC | TGAGTCCTAT | 120 |
| TGCCGGCTGC                                                      | TGGGAGCMAG                                          | GAGAGCCCTG | AGGAGTAGTC | ACTCAGTAGC | AGCTGACCGC | 180 |
| TGGGTCCACC                                                      | ATG AAC TGG AGT ATC TTT GAG GGA CTC CTG AGT GGG GTC | 229        |            |            |            |     |
|                                                                 | Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val |            |            |            |            |     |
|                                                                 | -45 -40 -35                                         |            |            |            |            |     |
| AAC AAG TAC TCC ACA GCC TTT GGG CGC ATC TGG CTG TCT CTG GTC TTC | 277                                                 |            |            |            |            |     |
| Asn Lys Tyr Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe |                                                     |            |            |            |            |     |
| -30 -25 -20                                                     |                                                     |            |            |            |            |     |
| ATC TTC CGC GTG CTG GTG TAC CTG GTG ACG GCC GAG CGT GTC TGG AGT | 325                                                 |            |            |            |            |     |
| Ile Phe Arg Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser |                                                     |            |            |            |            |     |
| -15 -10 -5                                                      |                                                     |            |            |            |            |     |
| GAT GAC CAC AAG                                                 | 337                                                 |            |            |            |            |     |
| Asp Asp His Lys                                                 |                                                     |            |            |            |            |     |

## (2) INFORMATION FOR SEQ ID NO: 275:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..287
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 37..119  
id T82645  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 129..176
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq SLFIYIFXTCSNT/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

```

ACTGTCCCAT TCCTCCCCCT ACAACACACA CACCTTTCAG GCAGGGASGN GATGAGCTTC 60
CAGCCCCAAG AGTGGAGGCT GCCACATCCT AACATASGKA KCTATTGRRR AGGAAKSAGT 120
GTGTATCT ATG ATT ATA TCT CTG TTC ATC TAT ATA TTT TTK ACA TGT AGC 170
Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Xaa Thr Cys Ser
 -15 -10 -5

AAC ACC TCT CCA TCT TAT CAA KGA ACT CAA CTC GGT CTG GGT CTC CCC 218
Asn Thr Ser Pro Ser Tyr Gln Xaa Thr Gln Leu Gly Leu Gly Leu Pro
 1 5 10

AGT GCC CAG TGG TGG CCT TTG ACA GGT AGG AGG ATG CAG TGC TGC AGG 256
Ser Ala Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg
 15 20 25 30

CTA TTT TGT TTT KTG TTA CAA 287
Leu Phe Cys Phe Xaa Leu Gln
 35

```

## (2) INFORMATION FOR SEQ ID NO: 276:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..156
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 40..195  
id AA227366  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..156
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 4..159  
id AA069390  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..152
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..144  
id AA248850  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..78  
id AA248912  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 70..114  
id AA248912  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 61..108
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4

seq LNSLSALAEAVG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

```
ATGGCTGTCA GAGGTGGGCG GCTTTGACCG AGAGGCTGCT GGAGCTCGTG TTTGGACGCG 60
ATG TTT CGT CTG AAC TCA CTT TCT CCT TTG GCA GAA CTG GCT GTG GGT 108
Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly
 -15 -10 -5

TCT CGA TGG TAC CAT GGA GGA TCA CAG CCC ATC CAG ATC CGG CGG AGA 156
Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Arg Arg
 1 5 10 15
```

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..330
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 69..301  
id R99696  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..98
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..70  
id R99696  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 206..330
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 164..288  
id W90165  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..209



(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 55..166  
id W90165  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 43..98  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..56  
id W90165  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 98..330  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 82..314  
id H91200  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 16..98  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..83  
id H91200  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 98..249  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 62..213  
id R06513  
est

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 238..288  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq TLRTWLCCAGSWA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

```
ACATACTTGC AGCTARAAC T AAATATTGCT GCTTGGGGAC CTCCTTCTAG CCTTAAATTT 60
CAGCTCATCA CCTTCACCTG CCTTGGTCAT GGCTCTGSCT AITCTCCTTG ATCCTTGCCA 120
TTTGCACCAG ACCTGGATTG CTAGCGICTC VATCTGGAGT GCGGCTGGTG GGGGGCCTGG 180
ACCGCTGTGA AGGGCGGGTG GAGGTGGAAC AGAAAGGCCA GTGGGGCACC GTGTGTG 240
ATG ACG GCT GGG ACA TTA AGG ACG TGG CTG TGT TGT GCC GGG AGC TGG 300
```

Met Thr Ala Gly Thr Leu Arg Thr Trp Leu Cys Cys Ala Gly Ser Trp  
 -15 -10 -5

GCT GTG GAG CTG CCA GCG GAA CCC CTA GTG GTA TTT TGT AWG AGC ACC 333  
 Ala Val Glu Leu Pro Ala Glu Pro Leu Val Val Phe Cys Xaa Ser Thr  
 1 5 10 15

AGC AGA AAA AGA GCA AAA GGT CTC ATC CAA TCA GTC 360  
 Ser Arg Lys Arg Ala Lys Gly Leu Ile Gln Ser Val  
 20 25

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..99)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
 region 99..196  
 id AA088690  
 est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(87..187)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
 region 12..112  
 id AA088690  
 est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 111..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
 seq RLLVILCVSVKAG/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

ACTACAGCAT GGCCACGTGG AGGCAGCGGC AGGAGAAAAA GCAGCTGGGC TTCTTCTGAA 60  
 CCCAAGCCCT CTCGACTGCC CCTATCCCTT GSAVCCCCAA CATACCTACA ATG CTG 116  
 Met Leu  
 GGG AGG CCC TGC TTC CAC TCC CCG CAG AGG CTT TTG GTC ATC CTC TGC 164

Gly Arg Pro Cys Phe His Ser Pro Gln Arg Leu Leu Val Ile Leu Cys  
-20 -15 -10

GTG TCA GTA AAA GCA GGC AGC ACG  
Val Ser Val Lys Ala Gly Ser Thr  
-5 1

188

## (2) INFORMATION FOR SEQ ID NO: 279:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 106..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 119..274  
id AA280906  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 15..112  
id AA280906  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 260..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 272..303  
id AA280906  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 224..375  
id HUM406F04B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 12..112  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..101  
id HUM406F04B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 106..140  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 94..128  
id HUM406F04B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 132..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 124..253  
id AA133362  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 5..92  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..88  
id AA133362  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 260..291  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 251..282  
id AA133362  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 106..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 94..249  
id N57260  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 10..92  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..83  
id N57260  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 260..291  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 247..278  
 id N57260  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 41..234  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
 region 42..235  
 id W25567  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 1..40  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 1..40  
 id W25567  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 194..277  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.2  
 seq LQFVLPVATQIQQ/EV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

```

AGGGGCGTTG GGAACGGTTG TAGGACGTTG CTCTTTATTC GTGAGTTTTC CATTTACCTC 60
CGCTGAACCT AGAGCTTCAG ACGCCCTATG GCGTCCGCCT CGACACCAAC CGGCGGCCTT 120
GAGCGCTGAG CAAGCAAAGG TGGTCCTCGC GGAGGTGATC CAGGCGTTCT CCGCCCCGGA 180
GAATGCAGTG CGC ATG GAC GAG GCT CGG GAT AAC GCC TGC AAC GAC ATG 229
 Met Asp Glu Ala Arg Asp Asn Ala Cys Asn Asp Met
 -25 -20

GGT AAG ATG CTG CAA TTC GTG CTG CCC GTG GCC ACG CAG ATC CAG CAG 277
Gly Lys Met Leu Gln Phe Val Leu Pro Val Ala Thr Gln Ile Gln Gln
-15 -10 -5

GAG GTT ATC AAA 289
Glu Val Ile Lys
1

```

## (2) INFORMATION FOR SEQ ID NO: 280:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 base pairs

(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 38..69  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..32  
id H56508  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 237..349  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.2  
seq LCALLGSAPSSMWA/GE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

```
AAACCTCCGT GGCTAGTCTT GACGTGGCGG GTTGCTTTCC AAAATGGCGC GGGTGCTGAA 60
GGCTGCAGCC GCDBAATGCC GTAGGTGAAT ACCGGGCACC GCCGACCTTC GCCATGGGAC 120
AGGGAGCGTG GGAACGGCGG TCGGGGGCGG AGGAKGCCTC GGTGTGGCCA AAGCACCTTG 180
ATCTAATGTC CTCCCCCGGG GGCGCGTTCC ACAGCAGCTG CTGTCACTTW KGGCAGAGGG 240
TGCCTTCCAG AAGCGCCACC GCTTAGTAGC GGGGATTGCB TTGTGC ATG AGT CCC 295
 Met Ser Pro
 -20
ATT TCG ATC CGA GAG CTG TGC GCC TTG GGC TCT GCA CCT TCC AGT ATG 343
Ile Ser Ile Arg Glu Leu Cys Ala Leu Gly Ser Ala Pro Ser Ser Met
 -15 -10 -5
TGG GCB GGA GAG 355
Trp Ala Gly Glu
 1
```

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 2..149  
id AA095592  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..105
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 219..306  
id T70757  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 163..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 37..129  
id H66541  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 163..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 37..129  
id R92835  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 172..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 14..97  
id H87601  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 52..90
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq MTDLLSASPWALT/IV

## (x) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

ACCAA5TTTG AGCACCTGGA AAGGGTTTAT GCTGACATCC CCTTCTGTGTT G ATG ACC 57  
Met Thr

```

GAC CTC TTA AGT GCC TCA CCC TGG GCC CTC ACT ATT GTT TCC AGT GAG 105
Asp Leu Leu Ser Ala Ser Pro Trp Ala Leu Thr Ile Val Ser Ser Glu
-10 -5 1 5

CTC CAC CTT GCT CCA TCC ATG ACC ACA GTG CAC CAG CTC GAG TCT CAA 155
Leu His Leu Ala Pro Ser Met Thr Thr Val Asp Gln Leu Glu Ser Gln
 10 15 20

GTG GAC AAT GTC ATC TTA CAG ACT GGA GAG AGT GCT AGT GAA TGC TTT 201
Val Asp Asn Val Ile Leu Gln Thr Gly Glu Ser Ala Ser Glu Cys Phe
 25 30 35

TGT CTT CAA TGC CCA TCT CTT GGA AAT ATT GAA GGT GGA GTA GCA ACC 249
Cys Leu Gln Cys Pro Ser Leu Gly Asn Ile Glu Gly Gly Val Ala Thr
 40 45 50

GGG CAY HGG 258
Gly His Xaa
55

```

## (2) INFORMATION FOR SEQ ID NO: 282:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..202
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 10..206  
id AA074428  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 196..257  
id AA074428  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..202
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..175



id AA158941  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 193..285  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 165..257  
id AA158941  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 37..202  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..166  
id AA148039  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 193..254  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 156..217  
id AA148039  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 250..285  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 214..249  
id AA148039  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 74..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..207  
id H72224  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 76..153  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.2  
seq LTCGPALVPRLWA/TC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

AAGAGGCTAG AAGCTGGATT CAGCGTGTCC GCGACCTCAC CTTTAGSTCC TGTGAGGGAC 60

GGCCCAGGTS GCAGG ATG TCC TGG TCT GGC CTT CTC CAT GGC CTC AAC ACG 111

Met Ser Trp Ser Gly Leu Leu His Gly Leu Asn Thr  
 -25 -20 -15

TCC CTA ACT TGT GGC CCA GCT CTG GTT CCC CGG CTC TGG GCT ACC TGC 159  
 Ser Leu Thr Cys Gly Pro Ala Leu Val Pro Arg Leu Trp Ala Thr Cys  
 -10 -5 1

TCC ATG GGT ACC CTG AAC CAG ATG CAC CGC CTG GGG CCC CCC AAG CGG 207  
 Ser Met Ala Thr Leu Asn Gln Met His Arg Leu Gly Pro Pro Lys Arg  
 5 10 15

CCG CCT CGG AAG CTG GGC CCC ACG GAA GGC CGG CCG CAG CTG AAG GGT 255  
 Pro Pro Arg Lys Leu Gly Pro Thr Glu Gly Arg Pro Gln Leu Lys Gly  
 20 25 30

GTG GTC CTG TGC ACG TTT ACC CGC AAC CGG 285  
 Val Val Leu Cys Thr Phe Thr Arg Asn Arg  
 35 40

## (2) INFORMATION FOR SEQ ID NO: 283:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
 region 1..206  
 id HSC3CC061  
 est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
 region 94..205  
 id H33976  
 est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..93
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
 region 1..45  
 id AA041823  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 49..93  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 1..45  
 id AA003782  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 25..93  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.1  
 seq LEAFSQAISAIQA/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

```

AAKAGCTGCT GTGGCGGCGG CAAC ATG GCG GAC GTG ATA AAT GTC AGT GTG 51
 Met Ala Asp Val Ile Asn Val Ser Val
 -20 -15

AAC CTG GAG GCC TTT TCC CAG GCC ATT AGT GCC ATC CAG GCG CTG CGA 99
Asn Leu Glu Ala Phe Ser Gln Ala Ile Ser Ala Ile Gln Ala Leu Arg
 -10 -5 1

TCC AGC GTG AGC AGG GTG TTC GAC TGC CTG AAG GAT GGG ATG CGG AAC 147
Ser Ser Val Ser Arg Val Phe Asp Cys Leu Lys Asp Gly Met Arg Asn
 5 10 15

AAG GAG ACG CTG GAG GGC CGG GAG AAG GCC TTT ATT GCG CAC TTC CAG 195
Lys Glu Thr Leu Glu Gly Arg Glu Lys Ala Phe Ile Ala His Phe Gln
 20 25 30

GAC AAC TTA CAT TCG GTC AAC CGG GAC CCA 225
Asp Asn Leu His Ser Val Asn Arg Asp Pro
 35 40

```

## (2) INFORMATION FOR SEQ ID NO: 284:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(210..340)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99

region 172..302  
id AA062591  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 109..204  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.1  
seq RLLSSLLLTMSNN/NP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```

AGACCCGATG GACCCCGGCG ACGCSCCATT TTGGAGTCTT CCCTAAGGAT CCTCTACCGG 60
CTTTTCGAGT CAGTGCTGCC GCCGCTGCCC GCGGCTTTGC AGAGCAGG ATG AAT GTG 117
 Met Asn Val
 -30

ATA GAC CAC GTG CGG GAC ATG GCG GCC GCG GGG CTG CAC TCC AAC GTG 165
Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu His Ser Asn Val
 -25 -20 -15

CGG CTC CTC AGC AGC TTG TTA CTT ACA ATG AGT AAT AAC AAC CCT GAG 213
Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn Asn Asn Pro Glu
 -10 -5 1

TTA TTC TCC CCA CCT CAG AAG TAC CAG CTT TTG GTG TAT CAT GCA GAT 261
Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val Tyr His Ala Asp
 5 10 15

TCT CTC TTT CAT GAT AAG GAA TAT CGG AAT GCT GTG AGT AAG TAT ACC 309
Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val Ser Lys Tyr Thr
 20 25 30 35

ATG GCT TTA CAG CAG AAG AAA GCG CTA AGT 339
Met Ala Leu Gln Gln Lys Lys Ala Leu Ser
 40 45

```

## (2) INFORMATION FOR SEQ ID NO: 285:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..41)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90

region 66..105  
id AA085310  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 70..117
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq ACLAWTAVRPSAC/CH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```
AAAGTGAGTT TGCGAACGGA GCAGCTGCTG CAGCAGGGCC CATGGCGGAC ACCCAGTACA 60
TCCTGCCCA ATG ACA TCG GCG TGT CTA GCC TGG ACT GCC GTG AGG CCT TCC 111
 Met Thr Ser Ala Cys Leu Ala Trp Thr Ala Val Arg Pro Ser
 -15 -10 -5

GCC TGC TGT CAC CCA CAG AGC GCC AAC TGG 141
Ala Cys Cys His Pro Gln Ser Ala Asn Trp
 1 5
```

## (2) INFORMATION FOR SEQ ID NO: 286:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(147..290)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 141..284  
id W12393  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 249..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..41  
id HSC2TF111  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 60..224

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4

seq VFGMSSSSGASNS/AF

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

```

ATCTCAACTT GGACTTGCAA TCACAGAACA TTTACCACCA TGAAGAGAA GGAAGTAGG 59
ATG AAT GGA AGT AGG ACT CTA ACG CAC AGC ATT AGT GAT GGA CAA CTT 107
Met Asn Gly Ser Arg Thr Leu Thr His Ser Ile Ser Asp Gly Gln Leu
-55 -50 -45 -40

CAA GGT GGC CAG TCC AAT AGT GAA CTA TTT CAG CAG GAG SSA CAG ACA 155
Gln Gly Gly Gln Ser Asn Ser Glu Leu Phe Gln Gln Glu Xaa Gln Thr
 -35 -30 -25

GCA CCA GCT CAA GTT CCT CAA GGC TTT AAT GTT TTT GGA ATG TCC AGT 203
Ala Pro Ala Gln Val Pro Gln Gly Phe Asn Val Phe Gly Met Ser Ser
 -20 -15 -10

TCC TCT GGT GCT TCA AAT TCA GCA CCA CAT CTT GGA TTT CAC TTA GGC 251
Ser Ser Gly Ala Ser Asn Ser Ala Pro His Leu Gly Phe His Leu Gly
 -5 1 5

AGC AAA GGA ACA TCT AGC CTT TCT CAA CAA ACT CCC GGG 290
Ser Lys Gly Thr Ser Ser Leu Ser Gln Gln Thr Pro Gly
10 15 20

```

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(68..194)

(C) IDENTIFICATION METHOD: blastn

```

(D) OTHER INFORMATION: identity 100
 region 204..330
 id N35493
 est

```

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(208..323)

(C) IDENTIFICATION METHOD: blastn

```

(D) OTHER INFORMATION: identity 100
 region 75..190
 id N35493

```

est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..79)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 318..395  
id N35493  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 186..233
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq FFLFLSFVLMYDG/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

```
ATAAAGAAG CAGCAAATAG AATTTCCAC AAAGTAAGTT GACTCTAAAT CTTAAGTATT 60
ACCTAGTTTT TTAAAGGTTT GAATATAATA ATGCAGTATT TGCAGTATAA AAAGGAAGCA 120
ATTTGTAGAG AATCATTTTG GTGCTCAAGT CTCTTAGCAG TGCCTTATTG CCTCATAGCA 180
AGAAG ATG CTG GGG TTT TTT TTG TTT TTG TCC TTT GTA TTA ATG TAT GAT 230
Met Leu Gly Phe Phe Leu Phe Leu Ser Phe Val Leu Met Tyr Asp
 -15 -10 -5

GGT TTG CGC CTT TTT GGC ATT CTT TCA ACA TGT CGT GTA CAT CAC ACC 278
Gly Leu Arg Leu Phe Gly Ile Leu Ser Thr Cys Arg Val His His Thr
 1 5 10 15

ATG AAT CAG TTC CTA ATT GAT ATA TCT AGC TTT ACC TCC CGA GTT CGG 326
Met Asn Gln Phe Leu Ile Asp Ile Ser Ser Phe Thr Ser Arg Val Arg
 20 25 30
```

## (2) INFORMATION FOR SEQ ID NO: 288:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 219..380
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 46..207

id N95583  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 213..335  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 46..162  
id AA283710  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 336..380  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 162..206  
id AA283710  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 240..320  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4  
seq SIKVLLQSALSLG/RS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```
AGTGGCTCTT CTGACCCAAG GCCCCGCCGT CCAGGTAGGG GGCTGTGGCC TCTAGGGATC 60
AGGGACTACT TACCTGCGAA TCCCGGTTGC CCGCCCGCCA RCACGTCCGK TYCCSTAARG 120
CARAMCGCCT KSGCTCCTGG CTGAACCGTC TTCTCAMCGT TTGSCGGAGT CTGANCTCCC 180
CACGCTTAGT CCACTAACGR AGCTATCCCT GCTCCTGMCC CACAGCTTCT AAGTGCCAG 239
ATG ATG GAG GAG CGT GCC AAC CTG ATG CAC ATG ATG AAA CTC AGC ATC 287
Met Met Glu Glu Arg Ala Asn Leu Met His Met Met Lys Leu Ser Ile
-25 -20 -15
AAG GTG TTG CTC CAG TCG GCT CTG AGC CTG GGC CGC AGC CTG GAT GCG 335
Lys Val Leu Leu Gln Ser Ala Leu Ser Leu Gly Arg Ser Leu Asp Ala
-10 -5 1 5
GAC CAT GCC CCC TTG CAG CAG TTC TTT GTA GTG ATG GAG CAC TGC TCA 383
Asp His Ala Pro Leu Gln Gln Phe Phe Val Val Met Glu His Cys Ser
10 15 20
```

## (2) INFORMATION FOR SEQ ID NO: 289:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 57..180

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 15..138  
id AA090170  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 226..286

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 184..244  
id AA090170  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 21..242

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90  
region 1..222  
id HSU46267  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 143..319

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90  
region 220..396  
id AA048294  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 149..286

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92  
region 139..276  
id AA118611  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 143..286

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92  
region 88..231  
id AAC63937  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 80..130  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
 seq XIVSAALLAFVQT/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

```

AGTTGCTCGG GCTGGGGGAT GAGAGCTGCA CCGCGCGGGA YAACTGCGCG GCGGCGCCCG 60
AMGGAGCAGA ACAGAGAGC ATG GAG CTG GAG AAG ATC CTC AGT GCA GCC CTC 112
 Met Glu Leu Glu Xaa Ile Val Ser Ala Ala Leu
 -15 -10

CTT GCC TTT GTC CAG ACA CAC CTC CCG GAG GCC GAC CTC AGT GGC TTG 160
Leu Ala Phe Val Gln Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu
 -5 1 10

GAT GAG GTC ATC TTC TCC TAT GTG CTK GGG GTC CTG GAG GAC CTG GGC 208
Asp Glu Val Ile Phe Ser Tyr Val Xaa Gly Val Leu Glu Asp Leu Gly
 15 20 25

CCC TCG GGC CCA TCA GAG GAG AAC TTC GAT ATC GAG CCT TTC ACT GAG 256
Pro Ser Gly Pro Ser Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu
 30 35 40

ATG ATG GAG GCC TAK GTG CCT GGC TTC GCC CAC ATC CCC AGG GGM ACA 304
Met Met Glu Ala Xaa Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr
 45 50 55

ATA GGG GAS ATG ATG 319
Ile Gly Xaa Met Met
 60

```

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 2..273  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 8..279  
 id T30552  
 est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 3..273  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 1..271  
                           id C14403  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 2..273  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 14..285  
                           id T30625  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 4..273  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 1..270  
                           id T32136  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 3..270  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 1..268  
                           id C14440  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 98..175  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
                           seq SLIPLFXFIGTGA/TG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

AGGAAGTCCG TAGTGCTCA TTGCGATAA TTTTAGCTT AGGGCCTKGT GGCTAGGKCG 60
GTTCTCTCCK KTCCAGTCGG AGACCTCTGC SGVRRRC ATG CTC CGC CAG ATC ATC 115
 Met Leu Arg Gln Ile Ile
 -25

GST CAG GCC AAG AAG CAT CCG AGC TTG ATC CCC CTC TTT KTA TTT ATT 163
Gly Gln Ala Lys Lys His Pro Ser Leu Ile Pro Leu Phe Xaa Phe Ile
-20 -15 -10 -5

GGR ACT GGA GCT ACT GGA GCA ACA CTG TAT CTC TTG CGT CTG GCA TTG 211
Gly Thr Gly Ala Thr Gly Ala Thr Leu Tyr Leu Leu Arg Leu Ala Leu
 1 5 10

TTC AAT CCA GRT GTT TGT TGG GAC AGA RRT AAC CCA GAG CCC TCG AAC 259
Phe Asn Pro Xaa Val Cys Trp Asp Arg Xaa Asn Pro Glu Pro Trp Asn

```

(2) INFORMATION FOR SEQ ID NO: 291:

(A) LENGTH: 336 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

[illegible]

(A) NAME/KEY: other  
(B) LOCATION: complement(230..332)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 117..219  
id R46866  
est

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 37..330  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.8  
seq WISLTCSLVVVDG/CG

|        |      |       |       |      |         |        |     |     |     |     |     |     |     |     |     |     |
|--------|------|-------|-------|------|---------|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AAGTGC | GGTG | GAGCC | AGGCG | TGGA | AAGTCGA | CACAAG | ATG | GTG | AAG | GAG | ACC | CAG |     | 54  |     |     |
|        |      |       |       |      |         |        | Met | Val | Lys | Glu | Thr | Gln |     |     |     |     |
|        |      |       |       |      |         |        |     |     |     |     | -95 |     |     |     |     |     |
|        |      |       |       |      |         |        |     |     |     |     |     |     |     |     |     |     |
| TAC    | TAT  | GAC   | ATC   | CTG  | GGC     | GTG    | AAG | CCC | AGC | GCG | TCC | CCG | GAG | AGA | TCA | 102 |
| Tyr    | Tyr  | Asp   | Ile   | Leu  | Gly     | Val    | Lys | Pro | Ser | Ala | Ser | Pro | Glu | Arg | Ser |     |
|        |      | -90   |       |      |         |        | -85 |     |     |     |     | -80 |     |     |     |     |
|        |      |       |       |      |         |        |     |     |     |     |     |     |     |     |     |     |
| AGA    | AGG  | CCT   | ATC   | GGA  | AGC     | TGG    | CGC | TCA | AGT | ACC | ACC | CGG | ACA | AGA | ACC | 150 |
| Arg    | Arg  | Pro   | Ile   | Gly  | Ser     | Trp    | Arg | Ser | Ser | Thr | Thr | Arg | Thr | Arg | Thr |     |
|        |      | -75   |       |      |         |        | -70 |     |     |     |     | -65 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CGG | ATG | AGG | GCG | AGA | AGT | TTA | AAG | TCA | TAT | CCC | AGG | CAT | ATG | AAG | TGC | 198 |
| Arg | Met | Arg | Ala | Arg | Ser | Leu | Asn | Ser | Tyr | Pro | Arg | His | Met | Lys | Cys |     |
| -60 |     |     |     |     | -55 |     |     |     |     | -50 |     |     |     |     | -45 |     |
| TTT | CAG | ATC | CAA | AGA | AAA | GGG | ATG | TTT | ATG | ACC | AAG | GCG | GAG | AGC | AGG | 246 |
| Phe | Gln | Ile | Gln | Arg | Lys | Gly | Met | Phe | Met | Thr | Lys | Ala | Glu | Ser | Arg |     |
|     |     |     |     | -40 |     |     |     |     | -35 |     |     |     |     | -30 |     |     |
| CAA | TBV | AAG | AAG | GAG | GCT | CAG | GCA | CCC | CCA | GCT | TCT | CTT | CAC | CCA | TGG | 294 |
| Gln | Xaa | Lys | Lys | Glu | Ala | Gln | Ala | Ala | Pro | Ala | Ser | Leu | His | Pro | Trp |     |
|     |     |     | -25 |     |     |     |     | -20 |     |     |     |     | -15 |     |     |     |
| ACA | TCT | TTG | ACA | TGT | TCT | TTG | GTG | GTG | GTG | GAC | GGA | TGC | GGG |     |     | 336 |
| Thr | Ser | Leu | Thr | Cys | Ser | Leu | Val | Val | Val | Asp | Gly | Cys | Gly |     |     |     |
|     |     | -10 |     |     |     |     | -5  |     |     |     |     | 1   |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

```
(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 18..194
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 2..178
 id W25476
 est
```

```
(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 206..359
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 193..346
 id W25476
 est
```

```
(ix) FEATURE:
```

|     |                        |                                                    |
|-----|------------------------|----------------------------------------------------|
| (A) | NAME/KEY:              | other                                              |
| (B) | LOCATION:              | 359..396                                           |
| (C) | IDENTIFICATION METHOD: | blastn                                             |
| (D) | OTHER INFORMATION:     | identity 94<br>region 347..384<br>id W25476<br>est |

(IX) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..278  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 19..276  
id HUM179H07B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 279..379  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 278..378  
id HUM179H07B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 17..175  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 27..185  
id AA002128  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 171..292  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 182..303  
id AA002128  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 358..396  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 373..411  
id AA002128  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 325..358  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 339..372  
id AA002128  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 204..396  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 186..378  
id AA253291  
est

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 251..359  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 234..342  
id W45609  
est

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: 59..166  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.8  
seq RALSTXLFGSIRG/AA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AGTGCGCAGA CGCAGGGGTC GGCGCCGGGT GAGAGCGTGC GGCCGGATTG ACCACAAC | 58  |
| ATG GCA AAT CTT TTT ATA AGG AAA ATG GTG AAC CCT CTG CTC TAT CTC | 106 |
| Met Ala Asn Leu Phe Ile Arg Lys Met Val Asn Pro Leu Leu Tyr Leu |     |
| -35 -30 -25                                                     |     |
| AGT CGT CAC ACG GTG AAG CCT CGA GCC CTC TCC ACA NTT CTA TTT GGA | 154 |
| Ser Arg His Thr Val Lys Pro Arg Ala Leu Ser Thr Xaa Leu Phe Gly |     |
| -20 -15 -10 -5                                                  |     |
| TCC ATT CGA GGT GCA GCC CCC GTG GCT GTG GAA CCC GGG GCA GCA GTG | 202 |
| Ser Ile Arg Gly Ala Ala Pro Val Ala Val Glu Pro Gly Ala Ala Val |     |
| 1 5 10                                                          |     |

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CGC TCA CTT CTC TCA CCC GGC CTC CTG CCC CAT CTG CTG CCT GCG CTG | 250 |
| Arg Ser Leu Leu Ser Pro Gly Leu Leu Pro His Leu Leu Pro Ala Leu |     |
| 15 20 25                                                        |     |
| GGG TTC AAA AAC AAG ACT GTC CTT AAG AAG CGC TGC AAG GAC TGT TAC | 298 |
| Gly Phe Lys Asn Lys Thr Val Leu Lys Lys Arg Cys Lys Asp Cys Tyr |     |
| 30 35 40                                                        |     |
| CTG GTG AAG AGG CGG GGT CGG TGG TAC GTC TAC TGT AAA ACC CAT CCG | 346 |
| Leu Val Lys Arg Arg Gly Arg Trp Tyr Val Tyr Cys Lys Thr His Pro |     |
| 45 50 55 60                                                     |     |
| AGG CAC AAG CAG AGA CAC ATG TAN ACC CTT TCC CTC CAG AGT CAC GCA | 394 |
| Arg His Lys Gln Arg His Met Xaa Thr Leu Ser Leu Gln Ser His Ala |     |
| 65 70 75                                                        |     |
| CAA                                                             | 397 |
| Gln                                                             |     |

## (2) INFORMATION FOR SEQ ID NO: 293:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 115..216
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 41..142  
id H64274  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 74..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..43  
id H64274  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 115..216
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 36..137  
id R16956  
est



## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..33  
id R16956  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 123..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 57..148  
id W04201  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 4..57  
id W04201  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 123..190
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 50..117  
id N76590  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 2..43  
id N76590  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(107..195)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 323..411  
id N70265  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 106..201
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq RIHLCQRSPGSQG/VR

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

```

ACCCTGCCTC ATGCAGCCTA TCGGCTAGCT TTTAGGGTCC GCGGTTGGTC AKACCGGAGC 60
ACTTGGCCTG AAGACCTGGA ATTGGYGACT TCGATATTAA CAAGG ATG GCG GCG GCC 117
 Met Ala Ala Ala
 -30

GCA GCA AGT CGA GGA KTC GGG GCA AAG CTG GGC CTG CGT GAN ATT CGC 165
Ala Ala Ser Arg Gly Xaa Gly Ala Lys Leu Gly Leu Arg Xaa Ile Arg
-25 -20 -15

ATC CAC TTA TGT CAG CGC TCG GCG GGC AGC CAG GGC GTC AGG GAC TTC 213
Ile His Leu Cys Gln Arg Ser Pro Gly Ser Gln Gly Val Arg Asp Phe
-10 -5 1

ATT 216
Ile
5

```

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..279)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..279  
id M85423  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(196..289)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 466..559  
id AA126476  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(133..194)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 560..621  
id AA126476  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(105..137)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 616..648  
id AA126476  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 152..292  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..141  
id R33928  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 160..292  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 14..146  
id H67425  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 161..292  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..132  
id W04820  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 101..232  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq IALTLPMSLSRA/AG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

```
AACTTCTTCA TCTTGGTGGT CCTTGCCCAG TTATTTTGCC TCATTAGACA TCAAGAAATG 60
GAGAAAGACT GAAAGTTAAT ATCTTAAGTG CTTGTCTTTC ATG TTT CCT TCT TGT 115
 Met Phe Pro Ser Cys
 -40
TAT TTA TGC TAT TCT CTT TGT GGC TCC ATT CTT CTT TCA ATC TTC TCA 163
Tyr Leu Cys Tyr Ser Leu Cys Gly Ser Ile Leu Leu Ser Ile Phe Ser
-35 -25
GCT TAT AAC CGT CTT TCC CTT ATG CTA AGG ATA GCC CTT ACA CTC ATC 211
```

```

Ala Tyr Asn Arg Leu Ser Leu Met Leu Arg Ile Ala Leu Thr Leu Ile
 -20 -15 -10

CCA TCT ATG CTG TCA AGG GCT GCT GGT TGG TGC TGG TAC AAG GAG CCC 259
Pro Ser Met Leu Ser Arg Ala Ala Gly Trp Cys Trp Tyr Lys Glu Pro
 -5 1 5

ACT CAG CAG TTT TCT TAC CTT TGC CTG CCC TGC GGG 295
Thr Gln Gln Phe Ser Tyr Leu Cys Leu Pro Cys Gly
 10 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 295:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(9..318)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 36..345  
id R32875  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(52..318)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 35..301  
id N69845  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(9..52)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 302..345  
id N69845  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(39..318)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 46..325  
id H20723

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(30..318)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 35..323  
 id HSC3JH072  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(65..318)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 43..296  
 id R02144  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 125..304  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq QLXFLYFVCCIFQ/DV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

```

AAMAAGCTCC CAGCCTCCAG AGGCTCTCAA TGAAGAGTCA CCTTCATGGT CGTCTYCAGG 60
AACAGGACGG ATGAMGAAGG GGTGGGGTTA AGACTCAGGG GCACCTGAGG GTCTGAGCCC 120
CCTT ATG AGT ACC CAA GAM GGA CTG TCT ATG CAT GCA CAC CCA CAA GCC 169
Met Ser Thr Gln Xaa Gly Leu Ser Met His Ala His Pro Gln Ala
-60 -55 -50

TAT ACA CCA TTT ATA TAC CTA CAC GCA CGC AAG AGA CGC GGA GAG ATA 217
Tyr Thr Pro Phe Ile Tyr Leu His Ala Arg Lys Arg Arg Gly Glu Ile
-45 -40 -35 -30

GGC GAT GCA GAC TCG CGA TTC AAT GAT CGA TAT GCT CAT AAR AGT GCT 265
Gly Asp Ala Asp Ser Arg Phe Asn Asp Arg Tyr Ala His Lys Ser Ala
-25 -20 -15

CAA TTA TMT TTT CTG TAT TTT GTA TGC TGT ATT TTC CAA GAC GTA TAT 313
Gln Leu Xaa Phe Leu Tyr Phe Val Cys Cys Ile Phe Gln Asp Val Tyr
-10 -5 1

TAT KTN 319
Tyr Xaa
5

```

## (2) INFORMATION FOR SEQ ID NO: 296:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 base pairs  
 (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(1..170)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 118..287  
id AA035134  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(1..170)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 116..285  
id N54275  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(1..170)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 119..288  
id AA088715  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(19..170)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 115..266  
id N78023  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(12..133)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 157..278  
id AA100730  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(127..170)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 119..162  
id AA100730

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 56..118
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq SSCSCSLISFTRG/DK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

```
ATCTTAGTGC CTTTATCTGT CTTTATGTCT TGGGGTTGGG GTAGGTAGAT ACCAA ATG 58
 Met
AAA CAC TTT CAG GAC CTT CCT TCC TCT TGC AGT TGT TCT TTA ATC TCC 105
Lys His Phe Gln Asp Leu Pro Ser Ser Cys Ser Cys Ser Leu Ile Ser
-20 -15 -10 -5
TTT ACT AGA GGA GAT AAA TAT TTT GCA TAT AAT GAA GAA ATT TTT CTA 154
Phe Thr Arg Gly Asp Lys Tyr Phe Ala Tyr Asn Glu Glu Ile Phe Leu
 1 5 10
GTA TAT AAC GCA GAC CAG 172
Val Tyr Asn Ala Asp Gln
 15
```

## (2) INFORMATION FOR SEQ ID NO: 297:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(29..369)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 103..443  
id W26961  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(383..424)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 48..89  
id W26961  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(34..369)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 100..435  
id W26018  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(383..424)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 45..86  
id W26018  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(200..369)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 111..230  
id W26871  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(143..200)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 281..338  
id W26871  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(383..424)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 56..97  
id W26871  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(94..123)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 361..390  
id W26871  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(119..369)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 104..354  
id W26098



est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(393..424)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 49..90  
 id W26098  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 31..302  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 1..272  
 id N99777  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 302..369  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
 region 273..340  
 id N99777  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 155..340  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq SILGIISVPLSIG/YC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

```

AGTGAAAAGA AGATGCCTAG AGAATGGCAA TTAAAAAGAA AAAGATATAC TTGTTTTGCC 60
CCTTGACCTG ACCGACACTG GTTCCCATGA AGCGGCTACC AAAGCTGTTT TCCAGGAGTT 120
TGGTAGAATC GACATTCIGG TCAACAATGG TGGA ATG TCC CAG CGT TCT CTG TGC 175
 Met Ser Gln Arg Ser Leu Cys
 -60

ATG GAT ACC AGC TTG GAT GTC TAC AGA RAG CTA ATA GAG CTT AAC TAC 223
Met Asp Thr Ser Leu Asp Val Tyr Arg Xaa Leu Ile Glu Leu Asn Tyr
-55 -50 -45 -40

TTA GGG ACG GTG TCC TTG ACA AAA TGT GTT CTG CCT CAC ATG ATC GAG 271
Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His Met Ile Glu
-35 -30 -25

AGG AAG CAN KKA AAG ATT GTT ACT GTG AAT AGC ATC CTG GGT ATC ATA 319
Arg Lys Xaa Xaa Lys Ile Val Thr Val Asn Ser Ile Leu Gly Ile Ile
-20 -15 -10

TCT GTA CCT CTT TCC ATT GGA TAC TGT GCT AGC RAG CAT GCT CTS HGG 367
Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Xaa His Ala Leu Xaa

```

-5

1

5

GGT TTT TTT AAT RDH CTT CGA ACA GAG CTT GCC ACA TAC CCA GGT ATA 415  
Gly Phe Phe Asn Xaa Leu Arg Thr Xaa Leu Ala Thr Tyr Pro Gly Ile  
10 15 20 25  
ATA GTT TCT 424  
Ile Val Ser

## (2) INFORMATION FOR SEQ ID NO: 298:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 179..348
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 160..329  
id AA159241  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..184
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 83..164  
id AA159241  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 383..437
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 366..420  
id AA159241  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..66
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..46  
id AA159241  
est

WO 99/06550

326

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..383
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 324..365  
id AA159241  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..102
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 47..83  
id AA159241  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..215
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 81..193  
id AA076222  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 216..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 195..308  
id AA076222  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..102
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..81  
id AA076222  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 390..437
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 374..421  
id AA076222  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 324..349  
id AA076222

est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 241..443  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 202..404  
id AA149750  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 40..215  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..176  
id AA149750  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 241..443  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 181..383  
id W63593  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 63..184  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 3..124  
id W63593  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 179..243  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 120..184  
id W63593  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 320..438  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 267..385  
id AA130386  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 216..328  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98

region 164..276  
id AA130386  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 103..215  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 50..162  
id AA130386  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 82..375  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq LALRTSWISSVCS/VT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

```

AAGTGACGCG GCCCAAGGGC GGAAGTGAGA AAGTTGTCTG CGTCTCGAGG CGAGTTGGCG 60
GACTGTGCGC GCGGCGGGGC G ATG GGG GGC TCG GGC AGT CGC CTG TCC AAG 111
 Met Gly Gly Ser Gly Ser Arg Leu Ser Lys
 -95 -90

GAG CTG CTG GCC GAR TAC CAG GAC TTG ACG TTC CTG ACG AAG CAG GAG 159
Glu Leu Leu Ala Glu Tyr Gln Asp Leu Thr Phe Leu Thr Lys Gln Glu
 -85 -75

ATC CTC CTA GCC CAC AGG CGG TTT TGT GAG CTG CTT CCC CAG GAG CAG 207
Ile Leu Leu Ala His Arg Arg Phe Cys Glu Leu Leu Pro Gln Glu Gln
 -70 -60

CGG ASK NGG AGT CGT CAC TTC GGG CAC AAG TGC CCT TCG AGC AGA TTC 255
Arg Xaa Xaa Ser Arg His Phe Gly His Lys Cys Pro Ser Ser Arg Phe
 -55 -45

TCA GCE TTC CAG AGC TCA AGG CCA ACC CCT TCA AGG AGC GAA TCT GCA 303
Ser Ala Phe Gln Ser Ser Arg Pro Thr Pro Ser Arg Ser Glu Ser Ala
 -40 -25

GGG TCT TCT CCA CAT CCC CAG CCA AAG ACA GCC TTA GCT TTG AGG ACT 351
Gly Ser Ser Pro His Pro Gln Pro Lys Thr Ala Leu Ala Leu Arg Thr
 -20 -10

TCC TGG ATC TCC TCA GTG TGT TCA GTG ACA CAG CCA CGC CAG ACA TCA 399
Ser Trp Ile Ser Ser Val Cys Ser Val Thr Gln Pro Arg Gln Thr Ser
 -5 1 5

AGT CCC ATT ATG CCT TCC GCA TCT TTG ACT TTG ATG ATG ACG 441
Ser Pro Ile Met Pro Ser Ala Ser Leu Thr Leu Met Met Thr
 10 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 299:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..162
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 9..169  
id N76992  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 162..280
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 168..286  
id N76992  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 8..119  
id W39234  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..280
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 176..283  
id W39234  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..162
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 118..167  
id W39234  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..160
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 1..141  
id R06371  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 193..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 173..260  
id R06371  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 159..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 138..174  
id R06371  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 20..159  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..140  
id R06399  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 161..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 141..260  
id R06399  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 27..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..139  
id AA043154  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 166..280  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 141..255  
id AA043154  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 132..215  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.6  
 seq PLSDSWALLPASA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

```

AACAACTTCC GGCCCCACTG AGCGGTGTCC TGACCCGATT ACAGCTAGGT AGTGGAGCGC 60
CGCTGCTTAC CTGGGTGCAG GACACAGCCG GAGTGGCTGG GGGAGCTCCG CGCCGCCGGA 120
CGCCCGTGAC C ATG TGG AGG CTG CTG GCT CGC GCT AGT GCG CCG CTC CTG 170
 Met Trp Arg Leu Leu Ala Arg Ala Ser Ala Pro Leu Leu
 -25 -20

CGG GTG CCC TTG TCA GAT TCC TGG GCA CTC CTC CCC GCC AGT GCT GGC 218
Arg Val Pro Leu Ser Asp Ser Trp Ala Leu Leu Pro Ala Ser Ala Gly
-15 -10 -5 1

GTA AAG ACA CTG CTC CCA GTA CCA AGT TTT GAA GAT GTT TCC ATT CCT 266
Val Lys Thr Leu Leu Pro Val Pro Ser Phe Glu Asp Val Ser Ile Pro
 5 10 15

GAA AAA CCC AAG CTA CTG 284
Glu Lys Pro Lys Leu Leu
 20

```

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 169..332  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 163..326  
                           id H71676  
                           est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 92..170  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 87..165  
                           id H71676  
                           est



## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 20..85  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 18..83  
                           id H71676  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 334..364  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 330..360  
                           id H71676  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 264..376  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 3..115  
                           id AA020192  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 6..347  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.6  
                           seq ATFVTQALIQXYA/RI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

```

AAAAA ATG GCG GAT CAT GTG CAG AGC CTG GCC CAA CTA GAG AAT CTG TGC 50
 Met Ala Asp His Val Gln Ser Leu Ala Gln Leu Glu Asn Leu Cys
 -110 -105 -100

AAA CAG CTG TAT GAA ACC ACA GAC ACA RSC AST CGG AGC TCC SAG GCA 98
Lys Gln Leu Tyr Glu Thr Thr Asp Thr Xaa Xaa Arg Ser Ser Xaa Ala
 -95 -90 -85

GAG AAA GCS TTG GTT GAR TTT ACC AAC AGC CCT GAT TGC CTG AGC AAG 146
Glu Lys Ala Leu Val Glu Phe Thr Asn Ser Pro Asp Cys Leu Ser Lys
 -80 -75 -70

TGC CAG CTA CTC CTC GAA AGA GGA AGT TCC TCT TAC TCC CAG TTA CTG 194
Cys Gln Leu Leu Leu Glu Arg Gly Ser Ser Ser Tyr Ser Gln Leu Leu
 -65 -60 -55

GCA GCT ACA TGC CIT ACC AAG CTT GTA TCA CGC ACA AAC AAC CCC CTA 242
Ala Ala Thr Cys Leu Thr Lys Leu Val Ser Arg Thr Asn Asn Pro Leu
 -50 -45 -40

CCA TTG GAA CAG CGA ATA GAT ATT CGG AAC TAT GTG CTC AAC TAS CTT 290
Pro Leu Glu Gln Arg Ile Asp Ile Arg Asn Tyr Val Leu Asn Xaa Leu
 -35 -30 -25 -20

```

GCC ACT CGG CCG AAG TGG GGT ACT TTC GTG ACA CAA GCA CTT ATT CAG 338  
Ala Thr Arg Pro Lys Leu Ala Thr Phe Val Thr Gln Ala Leu Ile Gln  
-15 -10 -5

TKA TAT GCC AGA ATC ACA AAA CTG GGC TGG TTT GAC 374  
Xaa Tyr Ala Arg Ile Thr Lys Leu Gly Trp Phe Asp  
1 5

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 2..222  
id H39781  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..173
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..158  
id AA017398  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 172..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 159..222  
id AA017398  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..220  
id AA059110  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 17..235  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 1..219  
                           id AA037143  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 56..235  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 56..235  
                           id R75754  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 14..55  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 15..56  
                           id R75754  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 62..226  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.6  
                           seq TCSVCCYLEFWLIA/IP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

```

AACACTTCCT GGTGGATCCG AGTGAGGCCA CGGGGTAGGG GTTGGCGCTC AGGCGGCGAC 60
C ATG GCG TAT CAC GGC CTC ACT GTG CCT CTC ATT GTG ATG AGC GTG TTC 109
 Met Ala Tyr His Gly Leu Thr Val Pro Leu Ile Val Met Ser Val Phe
 -55 - -50 -45 -40

TGG GGC TTC GTC GGC TTC TTG GTG CCT TGG TTC ATC CCT AAG GGT CCT 157
Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile Pro Lys Gly Pro
 -35 -30 -25

AAC CGG GGA GTT ATC ATT ACC ATG TTG GTG ACC TGT TCA GTT TGC TGC 205
Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys Cys
 -20 -15 -10

TAT CTC TTT TGG CTG ATT GCA ATT CCG GCC TGG 238
Tyr Leu Phe Trp Leu Ile Ala Ile Pro Ala Trp
 -5 1

```

## (2) INFORMATION FOR SEQ ID NO: 302:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 base pairs

(B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(397..432)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 283..318  
                           id H83411  
                           est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 54..227  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.5  
                           seq GGILMGSFQGTIA/GQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATATTTGCCC CTTACTTTAT CTTGTGCCTT GAGAAATTGC TGGGGAGAGA GGT ATG  | 56  |
| Met                                                             |     |
| TCC ACT GGG CAG CTG TAC AGG ATG GAG GAT ATA GGG CGT TTC CAC TCC | 104 |
| Ser Thr Gly Gln Leu Tyr Arg Met Glu Asp Ile Gly Arg Phe His Ser |     |
| -55 -50 -45                                                     |     |
| CAG CAG CCA GGT TCC CTC ACC CCA AGC TCA CCC ACT GTT GGG GAG ATT | 152 |
| Gln Gln Pro Gly Ser Leu Thr Pro Ser Ser Pro Thr Val Gly Glu Ile |     |
| -40 -35 -30                                                     |     |
| ATC TAC AAT AAC ACC AGA AAC ACA TTG GGG TGG ATT GGG GGT ATC CTT | 200 |
| Ile Tyr Asn Asn Thr Arg Asn Thr Leu Gly Trp Ile Gly Gly Ile Leu |     |
| -25 -20 -15 -10                                                 |     |
| ATG GGT TCT TTT CAG GGA ACC ATT GCT GGA CAA GGC ACA GGA GCC ACC | 248 |
| Met Gly Ser Phe Gln Gly Thr Ile Ala Gly Gln Gly Thr Gly Ala Thr |     |
| -5 1 5                                                          |     |
| TCC ATT TCT GAG CTC TSC AAG GGA CAA GAA CTA GAG CCA TCA GGG GCT | 296 |
| Ser Ile Ser Glu Leu Cys Lys Gly Gln Glu Leu Glu Pro Ser Gly Ala |     |
| 10 15 20                                                        |     |
| GGG CTC ACT GTG GCC CCA CCC CAA GCC GTC AGC CTC CAS GGA TCA CAC | 344 |
| Gly Leu Thr Val Ala Pro Pro Gln Ala Val Ser Leu Gln Gly Ser His |     |
| 25 30 35                                                        |     |
| CCT GCC TTG GCT GCT ACA GCT TTT TCA CTC CAS TGC CCT AGG GGA GTT | 392 |
| Pro Ala Leu Ala Ala Thr Ala Phe Ser Leu Xaa Cys Pro Arg Gly Val |     |
| 40 45 50 55                                                     |     |
| CAG CAS CTA ATG ATC TCT ATC TCT GAA CAT CTC TTC ATC CAT GCT     | 437 |

Gln Xaa Leu Met Ile Ser Ile Ser Glu His Leu Phe Ile His Ala  
60 65 70

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..321  
id T31485  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 42..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..311  
id HSC38B061  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..325
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 70..260  
id T66273  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 69..140
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 5..76  
id T66273  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 6..224

id R24829  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 236..275  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 243..282  
id R24829  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 50..318  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 10..278  
id HSC2LF071  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 282..332  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq RWWCFHLQAEASA/HP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

ATAATAATAT CTAAAAAGCT AAATTTTAAA TACCAGCTTT ACATAAATGA TTGTKGACTC 60  
TGGTCTGTKT CTGACACCTT TCCAGAAAAA AGTCAATTGT TCAGGTACAC CAAAGAGGAA 120  
GAAGAGCTGT GGAGGCCACC CTCTACAAAG CTTTATAGAA CTTCTGGATC TAACTCACAA 180  
ACAAGCTTCC AGAAGAGACT AGAGACCTTA GGCCAGSAGA TGAAGGAGTT CASTAGCAAA 240  
GTCACACCTG TCCAATTCCC TGAGCTTTGC TCACTCAGCT A ATG GSA TGG CAA AGG 296  
Met Gly Trp Gln Arg  
-15  
TGG TGG TGC TTT CAT CTT CAG GCA GAA GCC TCT GCC CAT CCC CCT CAA 344  
Trp Trp Cys Phe His Leu Gln Ala Glu Ala Ser Ala His Pro Pro Gln  
-10 -5 1  
GGG CTG CAG 353  
Gly Leu Gln  
5

## (2) INFORMATION FOR SEQ ID NO: 304:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 80..236

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95  
region 34..190  
id N34164  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 91..257

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 66..232  
id R89543  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 91..254

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 66..229  
id H59647  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 126..170

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.5  
seq VIFFACVVRVRDG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AGGTGACCTG GGCCGAGCCC TCCCGGTCCG CTAAGATTGC TGAGGAGGCG GCGGSTAGCT 60

GGCAGGCGCC GACTTCCGAA GGCCGCCGTC CGGGCGAGGT GTCCTCATGA CTTCTCTTGT 120

GGACC ATG TCC GTG ATC TTT TTT GCC TGC GTG GTA CGG GTA AGG GAT GGA 170

Met Ser Val Ile Phe Phe Ala Cys Val Val Arg Val Arg Asp Gly  
-15 -10 -5

CTG CCC CTC TCA GCC TCT ACT GAT TTT TAC CAC ACC CAA GAT TTT TTG 218

Leu Pro Leu Ser Ala Ser Thr Asp Phe Tyr His Thr Gln Asp Phe Leu  
1 5 10 15

GAA TGG AGG AGA CGG CTC AAG AGT TTA GCC TTG CGA CTG AAG 260

Glu Trp Arg Arg Arg Leu Lys Ser Leu Ala Leu Arg Leu Lys  
20 25 30

## (2) INFORMATION FOR SEQ ID NO: 305:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..210
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 29..195  
id R88607  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..135
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 16..134  
id AA035300  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..244
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 134..242  
id AA035300  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..244
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..207  
id AA147873  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(128..244)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 263..379  
id AA147836  
est

## (ix) FEATURE:

- (A) NAME/KEY: other



(B) LOCATION: complement(38..131)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 375..468  
                           id AAL47836  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 136..244  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 91..199  
                           id T69348  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 45..138  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 1..94  
                           id T69348  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 66..113  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.5  
                           seq TALAAXTWLGWVG/VR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

```

AATTAGCGCG TAACGCASAG ACTGCTTGCT GCGGCAGAGA CGCCAGAKGT GCAGCTCCAG 60
CAGCA ATG GCA GTG ACG GCG TTG GCG GCG MRG ACG TGG CTT GGC GTG TGG 110
 Met Ala Val Thr Ala Leu Ala Ala Xaa Thr Trp Leu Gly Val Trp
 -15 -10 -5

GGC GTG AGG ACC ATG CAA GCC CGA GGC TTC GGC TCG GAT CAG TCC GAG 158
Gly Val Arg Thr Met Gln Ala Arg Gly Phe Gly Ser Asp Gln Ser Glu
 1 5 10 15

AAT GTC GAC CGG GGC GCG GGC TCC ATC CGG GAA GCC GGT GGG GCC TTC 206
Asn Val Asp Arg Gly Ala Gly Ser Ile Arg Glu Ala Gly Gly Ala Phe
 20 25 30

GGA AAS AGA GAG CAG GCT GAA GAS SAA CGA TAT TTC 242
Gly Xaa Arg Glu Gln Ala Glu Xaa Xaa Arg Tyr Phe
 35 40

```

## (2) INFORMATION FOR SEQ ID NO: 306:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 151..402

(C) IDENTIFICATION METHOD: fasta

(D) OTHER INFORMATION: identity 100.0  
region 1..252  
id HSU21129  
vrt

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 155..402

(C) IDENTIFICATION METHOD: fasta

(D) OTHER INFORMATION: identity 99.6  
region 1..248  
id HSU18728  
vrt

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 131..402

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 1..272  
id H27256  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 161..402

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 31..272  
id W95921  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 296..402

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 141..247  
id C17793  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 151..252

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 1..102  
id C17793  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 174..402  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 1..229  
                           id AA180902  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 199..402  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 1..204  
                           id R58323  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 235..288  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 12  
                           seq FTLFLALIGGTSG/QY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

```

ACATGCCACA CCACAAGATC CCCACAATGA CATAACTCCA TTCAGAGACT GCGGTGACTG 60
GGCTGGGTCT CCCCACCCCC CCCTTCAGCT CTTGTATCAC TCAGAATCTG GCAGCCAGTT 120
CCGTCCTGAC AGAGTTCACA GCATATATTG GTGGATTCTT GTCCATAGTG CATCTGCTTT 180
AAGAATTAAC GAAAGCAGTG TCAAGACAGT AAGGATTCAA ACCATTTGCC AAAA ATG 237
 Met
AGT CTA AGT GCA TTT ACT CTC TTC CTG GCA TTG ATT GGT GGT ACC AGT 285
Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr Ser
 -15 -10 -5
GGC CAG TAC TAT GAT TAT GAT TTT CCC CTA TCA ATT TAT GGG CAA TCA 333
Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln Ser
 1 5 10 15
TCA CCA AAC TGT GCA CCA GAA TGT AAC TGC CCT GAA AGC TAC CCA AGT 381
Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro Ser
 20 25 30
GCC ATG TAC TGT GAT GAG CTG 402
Ala Met Tyr Cys Asp Glu Leu
 35

```

## (2) INFORMATION FOR SEQ ID NO: 307:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs  
 (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 120..272  
(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 96.1  
region 1..151  
id HSU21128  
vrt

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 124..272  
(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 96.0  
region 1..147  
id HSU18728  
vrt

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 141..272  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 40..171  
id H27256  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 100..136  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..37  
id H27256  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 141..272  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 40..171  
id W95921  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 141..245  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 52..156  
id AA093526

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 89..136  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
 region 2..49  
 id AA093526  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 145..272  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 1..128  
 id AA180902  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 141..223  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 20..102  
 id C17793  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 206..259  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 12  
 seq FTLFLALIGGTSG/QY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

```

ATAACTCCAT TCAGAGACTG GCGTGACTGG GCTGGGTCTC CCCACCCCCC CCTTCAGCTC 60
TTGTATGACT CAGAATCTGG CAGCCAGTTC CGTCCTGACA GAGTTCACAG CATATATTGG 120
TSGATTCTTG TCCAWAAGTG GVATCTGCTT TARGAWTTAA CGAAAGCAGT GTCAAGACAG 180
TAAGGATTCA AACCATTTCG CAAAA ATG AGT CTA AGT GCA TTT ACT CTC TTC 232
 Met Ser Leu Ser Ala Phe Thr Leu Phe
 -15 -10

CTG GCA TTG ATT GGT GGT ACC AGT GGC CAG TAC TAT GAT TGG 274
Leu Ala Leu Ile Gly Gly Thr Ser Gly Gln Tyr Tyr Asp Trp
 -5 1 5

```

## (2) INFORMATION FOR SEQ ID NO: 308:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 65..433

(C) IDENTIFICATION METHOD: fasta

(D) OTHER INFORMATION: identity 100.0  
region 1..369  
id HSU21128  
vrt

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 69..433

(C) IDENTIFICATION METHOD: fasta

(D) OTHER INFORMATION: identity 99.7  
region 1..365  
id HSU18728  
vrt

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 45..433

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 1..389  
id H27256  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 75..433

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 31..389  
id W95921  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 210..433

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99  
region 141..364  
id C17793  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 65..166

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98  
region 1..102  
id C17793  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 88..433  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 1..346  
 id AA180902  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 113..370  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 1..258  
 id R58323  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 149..202  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 12  
 seq FTLFLALIGGTSG/QY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

```

AGCTCTTGTA TCACTCAGAA TCTGGCAGCC AGTTCCTGCC TGACAGAGTT CACAGCATAT 60
ATTGGTGGAT TCTTGTCAT AGTGCATCTG CTTTAAGAAT TAACGAAAGC AGTGTCAGA 120
CAGTAAGGAT TCAAACCATT TGCCAAAA ATG AGT CTA AGT GCA TTT ACT CTC 172
 Met Ser Leu Ser Ala Phe Thr Leu
 -15

TTC CTG GCA TTG ATT GGT GGT ACC AGT GGC CAG TAC TAT GAT TAT GAT 220
Phe Leu Ala Leu Ile Gly Gly Thr Ser Gly Gln Tyr Tyr Asp Tyr Asp
-10 -5 1 5

TTT CCG CTA TCA ATT TAT GGG CAA TCA TCA CCA AAC TGT GCA CCA GAA 268
Phe Pro Leu Ser Ile Tyr Gly Gln Ser Ser Pro Asn Cys Ala Pro Glu
 10 15 20

TGT AAC TGC CCT GAA AGC TAC CCA AGT GCC ATG TAC TGT GAT GAG CTG 316
Cys Asn Cys Pro Glu Ser Tyr Pro Ser Ala Met Tyr Cys Asp Glu Leu
 25 30 35

AAA TTG AAA AGT GTA CCA ATG GTG CCT CCT GGA ATC AAG TAT CTT TAC 364
Lys Leu Lys Ser Val Pro Met Val Pro Pro Gly Ile Lys Tyr Leu Tyr
 40 45 50

CTT AGG AAT AAC CAG ATT GAC CAT ATT GAT GAA AAG GCC TTT GAG AAT 412
Leu Arg Asn Asn Gln Ile Asp His Ile Asp Glu Lys Ala Phe Glu Asn
 55 60 65 70

GTA ACT GAT CTG CAG TGG CTC GGG 436
Val Thr Asp Leu Gln Trp Leu Gly
 75

```

(2) INFORMATION FOR SEQ ID NO: 309:

## (2) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- ```
(A) NAME/KEY: other  
(B) LOCATION: 75..345  
(C) IDENTIFICATION METHOD: fasta  
(D) OTHER INFORMATION: identity 96.3  
                        region 1..269  
                        id HUMD3A07M5  
                        vrt
```

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 91..150
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq LLLLLLFFLLYMA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

AATTTGAATT	GGGGCGTGTC	TAGAAAGAGA	AGCCATAGTC	GGCGAGCAAC	GCTGGAGCAT	60
CCCGCTCTGG	TGCCGCTGCA	GCCGGCAGAG	ATG GTT GAG CTC ATG TTC CCG CTG		114	
			Met Val Glu Leu Met Phe Pro Leu			
			-20	-15		
TTG CTC CTC CTT CTG CCC TTC CTT CTG TAT ATG GCT GCG CCC CAA ATC					162	
Leu Leu Leu Leu Leu Pro Phe Leu Leu Tyr Met Ala Ala Pro Gln Ile						
	-10		-5	1		
AGG AAA ATG CTG TCC AGT GGG GTG TGT ACA TCA ACT GTT CAG CTT CCT					210	
Arg Lys Met Leu Ser Ser Gly Val Cys Thr Ser Thr Val Gln Leu Pro						
5		10		15	20	
GGG AAA GTA GTT GTG GTC ACA GGA GGT AAT ACA GGT ATC GGG AAG GAG					258	
Gly Lys Val Val Val Val Thr Gly Ala Asn Thr Gly Ile Gly Lys Glu						
	25		30		35	


```

ACA GCC AAA GAG CTG GCT CAG AGA GGA GCT CGA GTA TAT KTA GGT TNN      306
Thr Ala Lys Glu Leu Ala Gln Arg Gly Ala Arg Val Tyr Xaa Ala Xaa
      40                      45                      50

NGG GAT GTG GAA AAG GGG GAA TTG GTG GCC ARA GAG ATC CAG ACC ACC      354
Xaa Asp Val Glu Lys Gly Glu Leu Val Ala Xaa Glu Ile Gln Thr Thr
      55                      60                      65

ACA GGG AAN SAG CAG GTG TTG GTG CGG RAA CTG GAC CTG TCT GAT ACT      402
Thr Gly Xaa Xaa Gln Val Leu Val Arg Xaa Leu Asp Leu Ser Asp Thr
      70                      75                      80

AAG TCT ATT CGA GCT TTT GCT                                          423
Lys Ser Ile Arg Ala Phe Ala
      85                      90

```

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..303
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 96
region 1..171
id HSC1R
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 143..303
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 98
region 24..183
id HUMC1R
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 181..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 1..123
id T74375
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 170..213
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 1..44
id T64778
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 184..228
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.1
seq LLYLLVPALEFCRA/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

```
AAAAACTCAG ATCTTTTGT TATGCAAATA GTTCATTCCTT TCCAACATTC CTCCGGGAAT   60
GGTCCCCCCT CCACTCCACA GAAAACCCCTC CCCTCCCTGC TGTGCATGAC GCGGGCTCCC   120
TCTGSACACA GKGVMCRAAG ACGCTGTGGG GAKAGCCCCA GGATTCAACA CGGGCCTTGA   180
GAA ATG TGG CTC TTG TAC CTC CTG GTG CCG GCC CTG TTC TGC AGG GCA   228
Met Trp Leu Leu Tyr Leu Leu Val Pro Ala Leu Phe Cys Arg Ala
-15                      -10                      -5

GGA GGC TCC ATT CCC ATC CCT CAG AAG TTA TTT GGG GAG GTG ACT TCC   276
Gly Gly Ser Ile Pro Ile Pro Gln Lys Leu Phe Gly Glu Val Thr Ser
1           5           10          15

CCT CTG TTC CCC AAG CCT TAC CCC AAC GGG   306
Pro Leu Phe Pro Lys Pro Tyr Pro Asn Gly
20                      25
```

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 50..263
(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 99
region 1..214
id HSSPG28
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..263
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 99
region 1..189
id HSCRISP3G
vrt

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 51..146
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7
seq LLFLVAGLLPSFP/AN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

```

AATATATACG GCTCTAACCT TCTCTCTCTC CACCTTCCTT CTGTCAATAG ATG AAA      56
                                         Met Lys

CAA ATA CTT CAT CCT GCT CTG GAA ACC ACT GCA ATG ACA TTA TTC CCA      104
Gln Ile Leu His Pro Ala Leu Glu Thr Thr Ala Met Thr Leu Phe Pro
-30          -25          -20          -15

GTG CTG TTG TTC CTG GTT GCT GGG CTG CTT CCA TCT TTT CCA GCA AAT      152
Val Leu Leu Phe Leu Val Ala Gly Leu Leu Pro Ser Phe Pro Ala Asn
          -10          -5          1

GAA GAT AAG GAT CCC GCT TTT ACT GCT TTG TTA ACC ACC CAA ACA CAA      200
Glu Asp Lys Asp Pro Ala Phe Thr Ala Leu Leu Thr Thr Gln Thr Gln
          5          10          15

GTG CAA AGG GAG ATT GTG AAT AAG CAC AAT GAA CTG AGG AGA GCA GTA      248
Val Gln Arg Glu Ile Val Asn Lys His Asn Glu Leu Arg Arg Ala Val
          20          25          30

TCT CCC CCT GCC AAA      263
Ser Pro Pro Ala Lys
          35

```

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..147

(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 97
region 1..335
id HSU03877
vrt

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 213..467
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 232..486
id AA150097
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 35..204
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 55..224
id AA150097
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 43..467
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 56..480
id AA155808
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 43..404
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 73..434
id AA147966
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 395..467
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 424..496
id AA147966
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 51..467
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..417
id AA058479
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 70..405
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..336
 id W46890
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 394..425
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 326..357
 id W46890
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 52..102
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.9
 seq LFLTMLTLALVKS/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

```

AACTCCCCCTC GCTGCCCGGG CCCGGAGCGC ASSNGGCCGC ACAGATTCAC A ATG TTG      57
                                     Met Leu

AAA GCC CTT TTC CTA ACT ATG CTG ACT CTG GCG CTG GTC AAG TCA CAG      105
Lys Ala Leu Phe Leu Thr Met Leu Thr Leu Ala Leu Val Lys Ser Gln
-15                               -10                               -5                               1

GAC ACC GAA GAA ACC ATC ACG TAC ACG CAA TGC ACT GAC GGA TAT GAG      153
Asp Thr Glu Glu Thr Ile Thr Tyr Thr Gln Cys Thr Asp Gly Tyr Glu
                    5                               10                               15

TGG GAT CCT GTG AGA CAG CAA TGC AAA GAT ATT GAT GAA TGT GAC ATT      201
Trp Asp Pro Val Arg Gln Gln Cys Lys Asp Ile Asp Glu Cys Asp Ile
                20                               25                               30

GTC CCA GAC GCT TGT AAA GGT GGA ATG AAG TGT GTC AAC CAC TAT GGA      249
Val Pro Asp Ala Cys Lys Gly Met Lys Cys Val Asn His Tyr Gly
                35                               40                               45

GGA TAC CTC TGC CTT CCG AAA ACA GCC CAG ATT ATT GTC AAT AAT GAA      297
Gly Tyr Leu Cys Leu Pro Lys Thr Ala Gln Ile Ile Val Asn Asn Glu
                50                               55                               60                               65

CAG CCT CAG CAG GAA ACA CAA CCA GCA GAA GGA ACC TCA GGG GCA ACC      345
Gln Pro Gln Gln Glu Thr Gln Pro Ala Glu Gly Thr Ser Gly Ala Thr
                    70                               75                               80

ACC GGG GTT GTA GCT GCC DNC AGC ATG GCA ACC AGT GBA GTG TTG MNN      393
Thr Gly Val Val Ala Ala Xaa Ser Met Ala Thr Ser Xaa Val Leu Xaa
                    85                               90                               95

GGG GGT GGT TTT GTG GCC ACT GCT GCT GCA GTC GCA GGC CCT GAA ATG      441
Gly Gly Gly Phe Val Ala Ser Ala Ala Ala Val Ala Gly Pro Gln Met
                100                               105                               110

```

CAG ACT GGC CGG AAT AAC TTT GTC
Gln Thr Gly Arg Asn Asn Phe Val
115 120

465

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..256
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 96
region 1..204
id HUMTCAYV
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..256
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 93
region 1..207
id MACTCRAAQ
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..256
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 94
region 1..204
id MACTCRAAR
vrt

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 50..115
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LLILWFHLCVSS/IL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

AATTTTGGCT GCAAAACGTT TTTCTGCTGT GGGTACSTGA GCAGGAAAC ATG GAG AAG 58
Met Glu Lys
-20

```

AAT CCT TTC GCA GCC CCA TTA CTA ATC CTC TGG TTT CAT CTT GAC TGC      106
Asn Pro Leu Ala Ala Pro Leu Leu Ile Leu Trp Phe His Leu Asp Cys
      -15                      -10                      -5

GTG AGC AGC ATA CTG AAC GTG GAA CAA AGT CCT CAG TCA CTG CAT GTT      154
Val Ser Ser Ile Leu Asn Val Glu Gln Ser Pro Gln Ser Leu His Val
      1                      5                      10

CAG GAG GGA GAC AGC ACC AAT TTC ACC TGC AGC TTC CCT TCC AGC AAT      202
Gln Glu Gly Asp Ser Thr Asn Phe Thr Cys Ser Phe Pro Ser Ser Asn
      15                      20                      25

TTT TAT GCC TTA CAC TGG TAC AGA TGG GAA ACT GCA AAA AGC CCC GAG      250
Phe Tyr Ala Leu His Trp Tyr Arg Trp Glu Thr Ala Lys Ser Pro Glu
      30                      35                      40                      45

GCC GTG      256
Ala Val

```

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..455
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 98.7
region 1..392
id HSU32907
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..415
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..278
id H09504
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 410..454
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 274..318
id H09504

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 160..455
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..296
id H17686
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 128..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 42..243
id AA247900
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 85..123
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..39
id AA247900
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 318..355
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 231..268
id AA247900
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 128..231
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 22..125
id R57541
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 231..274
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 124..167
id R57541
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 312..455
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99

region 1..144
id N87278
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 345..389
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq VVTIVILLCFCKA/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

```
AGCTGGGGCC ATGTAATT TA AACCTCTGA AAAGTGTGCT GCGGTCCGTG CACAGCATT 60
GTATAACGTG AGGCTGAAT GCAGCCCAT CTCTGGAGAA CTTCCTCACA CACCGCAGCM 120
AARGAGAAGG MCTGAAAGAC AACCTGGGT GCAGCCAGAG AGGTCCAGAT AGATGASCTT 180
GTGGCATCCA TTCCCAAST TCAGCCTAGG GACTCCACGT ACCCCAGCTG GGTCTCAT TG 240
TTCCAGAACT GCATTAGTTA AGATTACCCA GACTTGATT TCAAAGGAAT ACTTTCATTG 300
TTCCGTCTGT AACACGAAGT AATTGGGGCC AGCTGGATGT CAGG ATG CGT GTG GTT 356
                                     Met Arg Val Val
                                     -15

ACC ATT GTA ATC TTG CTC TGC TTT TGC AAA GCG GCT GAG CTG CGC AAA 404
Thr Ile Val Ile Leu Leu Cys Phe Cys Lys Ala Ala Glu Leu Arg Lys
-10 -5 1 5

GCA AGC CCA GGC AGT GTG AGA AGC CGA GTG AAT CAT GGC CGG GCG GGT 452
Ala Ser Pro Gly Ser Val Arg Ser Arg Val Asn His Gly Arg Ala Gly
10 15 20

GGA 455
Gly
```

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 45..438
(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 100
region 1..394

id HSU20350
vrt

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 87..438
(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 99
region 3..352
id HSU28934
vrt

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 132..401
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq LLFVATLFPWTHY/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

```

AAACTCTGCA AATAAAATGC TCTTAGAGGG AAGGAAAGGG AAATACTCGT CTCTGGTAAA      60
GTCTGAGCAG GACAGGGTGG CTGACTGGCA GATCCAGAGG TTCCCTGGC AGTCCACGCC      120
AGGCCTTCAC C ATG GAT CAG TTC CCT GAA TCA GTG ACA GAA AAC TTT GAG      170
           Met Asp Gln Phe Pro Glu Ser Val Thr Glu Asn Phe Glu
           -90                      -85                      -80

TAC GAT GAT TTG GCT GAG GCC TGT TAT ATT GGG GAC ATC GTG GTC TTT      218
Tyr Asp Asp Leu Ala Glu Ala Cys Tyr Ile Gly Asp Ile Val Val Phe
           -75                      -70                      -65

GGG ACT GTG TTC CTG TCC ATA TTC TAC TCC GTC ATC TTT GCC ATT GGC      266
Gly Thr Val Phe Leu Ser Ile Phe Tyr Ser Val Ile Phe Ala Ile Gly
           -60                      -55                      -50

CTG GTG GGA AAT TTG TTG GTA GTG TTT GCC CTC ACC AAC AGC AAG AAG      314
Leu Val Gly Asn Leu Leu Val Val Phe Ala Leu Thr Asn Ser Lys Lys
           -45                      -40                      -35                      -30

CCC AAG AGT GTC ACC GAC ATT TAC CTC CTG AAC CTG GCC TTG TCT GAT      362
Pro Lys Ser Val Thr Asp Ile Tyr Leu Leu Asn Leu Ala Leu Ser Asp
           -25                      -20                      -15

CTG CTG TTT GTA GCC ACT TTG CCC TTC TGG ACT CAC TAT TTG ATA AAT      410
Leu Leu Phe Val Ala Thr Leu Pro Phe Trp Thr His Tyr Leu Ile Asn
           -10                      -5                      1

GAA AAG GGC CTC CAC AAT GCC ATG TGC      437
Glu Lys Gly Leu His Asn Ala Met Cys
           5                      10

```

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids
(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -23..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.4
seq VLALLLVHYSNG/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Met Val Phe Val His Leu Tyr Leu Gly Asn Val Leu Ala Leu Leu Leu
-20 -15 -10

Phe Val His Tyr Ser Asn Gly Asp Glu Ser Ser Asp Pro Gly Pro Gln
-5 1 5

His Arg Ala
10

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -29..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.3
seq FLLCIFLICAALA/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Met Gly Met Cys Phe Ala Ala Glu Ser Asp Val Gln Met Phe Ile Ala
-25 -20 -15

Phe Leu Leu Cys Ile Phe Leu Ile Cys Ala Ala Leu Ala Ala Gln Lys
-10 -5 1

Ser Gly
5

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11
seq VLFLFLFWGVSLA/GS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Ala Val Arg Glu Leu Cys Phe Ser Arg Gln Arg Gln Val Leu Phe
-25 -20 -15

Leu Phe Leu Phe Trp Gly Val Ser Leu Ala Gly Ser Gly Phe Gly Arg
-10 -5 1 5

Tyr Ser Val Thr Gly
10

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7
seq LILLALATGLVGG/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
-15 -10 -5

Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser
1 5 10
Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
15 20 25 30
Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
35 40 45
Lys Pro Arg Tyr Gly
50

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: AMINO ACID

(11) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 10.7
seq LILLALATGLVGG/ET

seq LILLALATGLVGG/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
-15 -10 -5

Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Naa
1 5 10

Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
15 20 25 30

Ala Thr Leu Ile Ala Pro Arg Trp Leu
35

(2) INFORMATION FOR SEQ ID NO: 321:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: AMINO ACID

(11) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -30..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.6
seq SLLLAVLVFFFLFA/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

```

Met Arg Ser Cys Leu Trp Arg Cys Arg His Leu Ser Gln Gly Val Gln
-30          -25          -20          -15

Trp Ser Leu Leu Leu Ala Val Leu Val Phe Phe Leu Phe Ala Leu Pro
          -10          -5          1

Ser Xaa Xaa Xaa Xaa Xaa Gln Thr Lys Pro Ser Arg His Gln Arg Thr
          5          10          15

Glu Asn Ile Lys Glu Arg Ser Leu Xaa Ser Leu Ala Lys Pro Lys Ser
          20          25          30

Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr Ile Tyr Ala Glu Pro Val
          35          40          45          50

Pro Glu Asn Asn Ala Leu Asn Thr Gln Thr Gln Pro Lys Ala His Thr
          55          60          65

Thr Gly Asp Arg Arg Lys Gly
          70

```

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.6
seq XILLALATGLVGG/EI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

```

Met Arg Ile Leu Gln Xaa Ile Leu Leu Ala Leu Ala Thr Gly Leu Val

```

(ii) MOLECULE TYPE: PROTEIN

(v1) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -23..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.2
seq RCLLLALVAESSS/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

Met Ile Ala Cys Ser Ile Arg Glu Leu His Arg Cys Leu Leu Leu Ala
-20 -15 -10
Leu Val Ala Glu Ser Ser Ser Gln Thr His Gly
-5 1

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(v1) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.2
seq SLVLCLLSATVFS/LQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

Met Gly Pro Pro Ser Leu Val Leu Cys Leu Leu Ser Ala Thr Val Phe
-15 -10 -5
Ser Leu Gln Gly Gly Ser Ser Ala Phe Leu Ser His His Arg Pro Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9
seq AMWWLLWGVQLQX/XP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

```

Met Pro Gly Pro Arg Val Trp Gly Lys Tyr Leu Trp Arg Ser Pro His
-35                -30                -25                -20

Ser Lys Gly Cys Pro Gly Ala Met Trp Trp Leu Leu Leu Trp Gly Val
          -15                -10                -5

Leu Gln Xaa Xaa Pro Asn Pro Gly Leu Arg Pro Leu Gly Xaa Arg Ala
          1                5                10

Thr Pro Ala Ala Asp Ile Pro Arg Val Pro Arg Ala Val Trp Gln Arg
          15                20                25

Pro Arg Glu Gln His Gly His Gln Gly Ser Arg Gly Leu Cys Cys Glu
          30                35                40                45

Ala Arg Leu Pro Gly Leu Arg Pro Gly Ala Val Pro Gly Leu Cys Arg
          50                55                60

Gly Leu Cys His Asn Leu Ile Arg Arg Phe Gly Ser Lys Pro Leu Gly
          65                70                75

```

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8
seq LLTLALLGGPTWX/XX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met His Arg Pro Glu Ala Met Leu Leu Leu Thr Leu Ala Leu Leu
 -20 -15 -10

Gly Gly Pro Thr Trp Xaa Xaa Lys Met Tyr Gly Pro Gly Gly Gly Lys
 -5 1 5 10

Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr Gly Leu Arg
 15 20 25

Val Ser Val Gly Xaa Leu Leu Val Lys Ser Val Gln Val Lys Leu Gly
 30 35 40

Asp Ser Trp Asp Val Lys Leu Gly Gly Leu Arg Trp Glu Tyr Pro Gly
 45 50 55

Ser His Pro Ala Ala Arg Arg Ile His His Lys Ser Leu Cys Arg Phe
 60 65 70

Gln Ala Phe Leu
 75

(7) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6
 seq SVSLALLSGWVGS/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

Met Val Ser Val Ser Leu Ala Leu Leu Ser Gly Trp Val Gly Ser Arg
 -15 -10 -5 1

Gln Gly Gly Val Gly Leu Ser Thr Leu Val Thr Leu Gly Leu Val Ser
 5 10 15

Trp Cys Trp Arg Met Val Arg Thr Gln Ala Leu Glu Gly Phe Leu Ser
 20 25 30

Val Lys Tyr Tyr Ser Ala Phe Ser Ala Asp Leu
 35 40

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5
seq IVFLLLRVSPCLG/PS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

```

Met His Ile Phe Ser Ile Cys Cys Met Xaa Ser Glu Leu His Lys Met
      -45                      -40                      -35

Lys Ser Leu Ser Leu Gln Leu Ala Ser Glu Lys Arg Ser Leu Val Ala
      -30                      -25                      -20

Leu Val Glu Glu Ile Val Phe Leu Leu Leu Arg Val Ser Pro Cys Leu
      -15                      -10                      -5

Gly Pro Ser Xaa Lys Pro Arg
      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3
seq VSALLMAWFGVLS/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

```

Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val Leu
      -15                      -10                      -5

```

Ser Cys Val Gln Thr Gly
 1 5

(1) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3
seq LLLPLMLMSMVSS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Pro Leu Met Leu
 -20 -15 -10

Met Ser Met Val Ser Ser Ser Leu Xaa Pro Gly Val Ala Arg Gly His
 -5 1 5 10

Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Gln Gly Gly Leu
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3
seq LLLPLMLMSMVSS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

```

Met Lys Val Leu Ile Ser Ser Leu Leu Leu Leu Leu Pro Leu Met Leu
  -20                -15                -10

Met Ser Met Val Ser Ser Ser Leu Asn Pro Gly Val Ala Arg Gly His
  -5                1                5                10

Arg Asp Arg Gly Gln Ala Ser Arg Arg Trp Leu Gln Glu Gly Gly Gln
          15                20                25

Glu Cys Glu Cys Lys Asp Trp Phe Leu Arg Ala Pro Arg Arg Lys Phe
          30                35                40

Met Thr Val Ser Gly
          45

```

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.2
seq LLLQLSLPSPTS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

```

Met Leu Leu Leu Leu Gln Leu Ser Leu Pro Ser Pro Thr Ser Ser Pro
          -10                -5                1

```

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -17..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.1
 seq LSFKLLLLAVALG/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

Met Leu Lys Met Leu Ser Phe Lys Leu Leu Leu Leu Ala Val Ala Leu
 -15 -10 -5

Gly Phe Phe Glu Gly Asp Ala Lys Phe Gly Glu
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -22..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8
 seq LLTLALLGXXXWA/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu Leu
 -20 -15 -10

Gly Xaa Xaa Xaa Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly Gly Lys
 -5 1 5 10

Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr Gly Leu Arg
 15 20 25

Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln Val Lys Leu Gly
 30 35 40

Asp Ser Trp Asp Val
 45

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8
seq VSAVLCVCAAWC/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

```
Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Trp Cys
-15                      -10                      -5

Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly Gly Arg
 1              5              10              15

Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu Thr Thr Ile
      20              25              30

Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys Phe Arg Asp Asp
      35              40              45

Asp Tyr Phe Arg Thr Gly
      50
```

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.8
seq VLWLISFFTFDDG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

```
Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp
-15                      -10                      -5
```

Gly His Gly Gly Phe Leu Gly Lys Asn Asp Gly Ile Lys Thr Lys Lys
 1 5 10 15
 Glu Leu Ile Val Asn Lys Lys Lys His Leu Gly Leu Gly
 20 25

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7
seq ILLDLICLLFITACV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

Met Cys Ile Ile Leu Leu Asp Leu Ile Cys Leu Leu Phe Ile Thr Ala
 -15 -10 -5
 Cys Val Gly
 1

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -59..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq FMVFGSFFFLISC/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:


```

Met Asp Cys Ala Ser Ile Ser Val Lys Phe Thr Ser Met Ala Trp Met
      -55                -50                -45

His Asp Leu Ser Gln Phe Trp Ala Ser Arg Gly Glu Val Thr Asn Trp
      -40                -35                -30

Trp Pro Val Gly Gln Thr Ser Leu Pro Leu Phe Tyr Leu Ala Phe Met
      -25                -20                -15

Val Phe Gly Ser Phe Phe Pro Leu Ile Ser Cys Gln Pro Gly
      -10                -5                1

```

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq LVVLEFGITAGTG/AK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

```

Met Thr Ala Ser Pro Asp Tyr Leu Val Val Leu Phe Gly Ile Thr Ala
-20                -15                -10                -5

Gly Ala Thr Gly Ala Lys Leu Gly Ser Asp Glu Lys Glu Leu Ile Leu
      1                5                10

Leu Phe Trp Lys Val Val Asp Leu Ala Asn Lys Lys Val Gly Gln Leu
      15                20                25

His Glu Xaa Xaa Leu Asp Arg Ile Trp
      30                35

```

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: -15..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.6
 seq CVLVLAAGAVA/VF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

```

Met Val Cys Val Leu Val Leu Ala Ala Ala Ala Gly Ala Val Ala Val
-15              -10              -5              1
Phe Leu Ile Leu Arg Ile Trp Val Val Leu Arg Ser Met Asp Val Thr
      5              10              15
Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly Ser Gly Gly His
      20              25              30
Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser Asn Ala Tyr Ser
      35              40              45
Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met Ser Ala Thr
      50              55              60

```

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: -44..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.5
 seq LMIPLLLTPITA/TS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

```

Met Lys Lys Thr Gly Asp Gly Gly Thr Leu Ser Thr Glu Arg Ile Gly
      -40              -35              -30
Gly Ala Ala Leu Leu Ser Leu Leu Leu Lys Arg Met Lys Met Thr Leu
      -25              -20              -15

```

```

Met Ile Pro Leu Leu Leu Thr Pro Ile Thr Ala Thr Ser Thr Ser
  -10          -5          1
Arg Trp Pro Glu Ile Gly Val Val Ala Ile Arg Ser Gln Leu Arg Ala
  5          10          15          20
Leu His Thr Cys Gly Gln Glu Pro Val Pro Ala Met Gly Ser Glu Gly
          25          30          35
Ala Ala

```

(2) INFORMATION FOR SEQ ID NO: 343:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(1x) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.5
seq LTFLLQLLISSLP/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

```

Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu Gln Leu
  -20          -15          -10
Leu Leu Ile Ser Ser Leu Pro Arg Glu Tyr Thr Val Ile Asn Glu Ala
  -5          1          5
Cys Pro Gly Ala Glu Trp Xaa Ile Met Cys Arg Glu Cys Cys Glu Tyr
  10          15          20          25
Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu Val Val Gly Tyr
          30          35          40
Thr Ile Pro Cys Cys Arg Asn Glu Xaa Asn Glu Cys Asp Ser Cys Leu
          45          50          55
Ile His Pro Gly Cys Thr Ile Phe Glu Asn Cys Xaa Ser Cys Arg Asn
          60          65          70
Gly Ser Trp Gly Gly Thr Leu
          75          80

```

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq SLLFFLLLEGXT/EQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

```
Met Arg Xaa Lys Trp Lys Met Gly Gly Met Lys Tyr Ile Phe Ser Leu
   -25                      -20                      -15

Leu Phe Phe Leu Leu Leu Glu Gly Gly Xaa Thr Glu Gln Val Xaa His
   -10                      -5                      1                      5

Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu
           10                      15                      20

Arg Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn
           25                      30                      35

Cys Ile Cys Ser Glu Xaa Gly Asn Val Leu Cys Ser Arg Val Arg Cys
   40                      45                      50
```

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq VCIMLLLVTVSDC/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val Thr Val
 -15 -10 -5

Ser Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys
 1 5 10

Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg
 15 20 25

Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser
 30 35 40 45

His Lys Ile Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys
 50 55 60

Leu

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq SALLFSLCEAST/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu
 -20 -15 -10

Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro
 -5 1 5 10

Xaa Thr Asn Asn Phe Xaa Asp Xaa Glu Ala Ala Leu Lys Ala His
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq SALLPSLLCEAST/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

Met Ile Ala Ile Ser Ala Val Ser Ser Ala Leu Leu Phe Ser Leu Leu
-20 -15 -10
Cys Glu Ala Ser Thr Val Val Leu Leu Asn Ser Thr Asp Ser Ser Pro
-5 1 5 10
Pro Thr Asn Asn Phe Thr Asp Ile Glu Ala Ala Leu Lys Ala Gln Leu
15 20 25
Asp Ser Ala Asp Ile Pro Lys Ala Arg Arg Lys Arg Tyr Ile Ser Gln
30 35 40
Asn Asp Met Ile Ala Ile Leu Asp Tyr His Asn Gln Val Arg Gly Lys
45 50 55
Val Phe Pro Xaa Ala
60

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq LLTLVLCVAVAYE/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Asp Pro Asn Gly Gly Cys Cys Thr Leu Leu Thr Leu Val Leu Cys
-20 -15 -10

Val Ala Val Ala Tyr Glu Arg Gln Glu
 -5 1

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq LFTFSTSLPSSLSS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Glu Gly Glu Ile Tyr Phe Gln Val Phe Leu Ser Leu Phe Thr Phe
 -25 -20 -15 -10

Ser Thr Ser Leu Pro Ser Ser Leu Ser Ser Ser Ser Leu Ser Ser Ser
 -5 1 5

Asn Gly

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq FLCMLAAIDLALS/TS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
 -40 -35 -30

Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
 -25 -20 -15 -10

Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met
 -5 1

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq PWFLAPWCPGTQS/NR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met Arg Glu Thr Xaa Pro Leu Pro Lys Pro Leu Lys Asp Thr Ala Pro
 -40 -35 -30

Ser Ser His Gly Val Gly Ser Asp Ser Pro Ser Ala Thr Arg Pro Trp
 -25 -20 -15

Phe Leu Ala Pro Trp Cys Pro Gly Thr Gln Ser Asn Arg Ile Cys His
 -10 -5 1 5

Pro Pro Leu Ser Ser Pro Pro Asp Gln Ala Thr Cys Leu Arg Gly
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq VLVVLALRSLGRS/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

```

Met Asp Arg Pro Gly Ser Leu Ser Val Phe Gly Ser Leu Pro Ala Ser
-60                -55                -50                -45

Leu Gly Thr Trp Leu Ser Ser Pro Ala Trp Leu Val Asp Arg Pro Val
                -40                -35                -30

Arg Ser Ala His Pro Ser Ala Asn Ser Thr Gly Val Arg Met Ser Val
                -25                -20                -15

Leu Val Val Leu Ala Leu Arg Ser Leu Gly Arg Ser Cys Ser Leu Ser
                -10                -5                1

Gln Ala Ala Pro Ser Arg Trp Thr Arg Ser Asn Asp Ala Pro Gln Pro
 5                10                15                20

Pro Gly Ser Gln His Ile Phe His Thr Xaa Val Pro Gly
                25                30

```

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq VILLESYPSCCLC/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

```

Met His Tyr Phe Val Ala Gly Lys Val Ile Leu Leu Phe Ser Tyr Pro
-20                -15                -10

Ser Cys Cys Leu Cys Phe Leu Val Tyr Arg Arg Val Ser Xaa Leu Phe
-5                1                5                10

Lys Cys Phe Glu
                15

```

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq STVVVLQVLTQATS/QD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Asp Leu Asn Ser Ala Ser Thr Val Val Leu Gln Val Leu Thr Gln
 -15 -10 -5

Ala Thr Ser Gln Asp Thr Ala Val Leu Lys Pro Ala Glu Glu Gln Leu
 1 5 10

Lys Gln Trp Glu Thr Gln Pro Gly Phe Tyr Ser Val Leu Leu Asn Ile
 15 20 25

Phe Thr Asn His Gly
 30

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq FLCMLAAIDLALS/TS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

```

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile
-70                      -65                      -60

Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
-55                      -50                      -45

Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
-40                      -35                      -30

Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
-25                      -20                      -15                      -10

Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met
-5                      i

```

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -56..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq PLFFSCSISATHS/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

```

Met Tyr Arg Leu Ser Leu Ile Ala Gly Pro Gly Ser Tyr Pro Val Leu
-55                      -50                      -45

Arg Trp Gly Val Trp Asp Ile Pro Ser Ser Leu Val Gln Val Thr Tyr
-40                      -35                      -30                      -25

His Gln Pro Asn Leu Thr Thr Asn Leu Asp Leu Pro Leu Phe Phe Ser
-20                      -15                      -10

Cys Ser Ile Ser Ala Thr His Ser Cys Val Lys Pro Pro Ser Val Ile
-5                      1                      5

Ile Gly Ile Ser Ser Phe Leu Ser Phe Pro Tyr Gln Thr Leu Val
10                      15                      20

```

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq LCFELLLAVAMSFF/GS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu
-20 -15 -10

Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu
-5 1 5

Thr Arg Ala His Leu Leu Leu Lys Glu Lys Met Met Arg Leu Gly Gly
10 15 20

Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met
25 30 35 40

Thr Leu Lys Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe
45 50 55

Pro Pro Ser Met His Phe Phe Gln Ala Lys Trp
60 65

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq XLXXLLTPPPSYG/HQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

```

Met Pro Cys Ser Leu Thr Trp Arg Leu Pro Pro Arg Thr Cys Gln Xaa
-35          -30          -25          -20

Xaa Gly Leu Xaa Lys Ser Xaa Leu Xaa Xaa Leu Leu Thr Pro Pro Pro
          -15          -10          -5

Ser Tyr Gly His Gln Pro Gln Thr Gly Ser Gly Glu Ser Xaa Gly Ala
          1          5          10

Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys
          15          20          25

```

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8
seq LFLFLTSIAEXCS/TP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

```

Met Val Xaa Trp Leu Val Leu Phe Ala Leu Gln Ile Tyr Ser Tyr Xaa
-40          -35          -30

Ser Thr Arg Asp Gln Pro Ala Ser Arg Xaa Arg Leu Leu Phe Leu Phe
-25          -20          -15          -10

Leu Thr Ser Ile Ala Glu Xaa Cys Ser Thr Pro Tyr Ser Leu Leu Gly
          -5          1          5

Xaa Val Phe Thr Val Ser Phe Val Ala Leu Gly Val Leu Thr Leu Cys
          10          15          20

Lys Phe Tyr Leu Gln Gly Tyr Arg Ala Phe Met Asn Asp Pro Ala Met
          25          30          35

Asn Arg Gly Gly Ala
          40

```

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq LPDLXXXSLPVGA/WL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

```

Met Ala Arg His Gly Leu Pro Leu Leu Xaa Xaa Xaa Ser Leu Pro Val
    -15                -10                -5

Gly Ala Trp Leu
    1

```

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq ILYILWYCSVCSS/GS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

```

Met Val His Leu Arg Thr Gly Leu Met Leu Met Ser Ala Asp Arg Leu
    -35                -30                -25

Arg Thr Leu Tyr Tyr Thr Val Thr Ile Leu Tyr Ile Leu Trp Tyr Cys
    -20                -15                -10

Ser Val Cys Ser Ser Gly Ser Leu Leu Ser Thr Ser Ile Met Lys Lys
    -5                1                5                10

```

Arg Met

(2) INFORMATION FOR SEQ ID NO: 362:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq ILSTVTALTFAA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Arg Ala Leu
-15 -10 -5 1

Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser Glu Lys His Arg
5 10 15

Leu Glu Lys Cys Arg Glu Leu Glu Ser Ser His Ser Ala Pro Gly Ser
20 25 30

Thr Gln Gln
35

(2) INFORMATION FOR SEQ ID NO: 363:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: PROTEIN

(v1) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -23..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.5
 seq LTFLOXLLLISSLK/RE
```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

Met Glu Leu Gly Cys Trp Thr Gln Leu Gly Leu Thr Phe Leu Gln Xaa  
-20 -15 -10  
Leu Leu Ile Ser Ser Leu Xaa Arg Glu Tyr Thr Val Ile Asn Glu Ala  
-5 1 5  
Arg Lys  
10

## (2) INFORMATION FOR SEQ ID NO: 364:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4  
seq FLLCXSVFTDCKG/DV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Met Glu Leu Leu Arg Val Cys Ser Phe Phe Leu Leu Cys Xaa Ser Val  
-20 -15 -10  
Phe Thr Asp Cys Lys Gly Asp Val Leu Cys Val Lys Met Glu Gln Ser  
-5 1 5 10  
Gln Ile Cys Ala

## (2) INFORMATION FOR SEQ ID NO: 365:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate



## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq TWFLLLPPGQCRA/VG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Ile Val Arg Pro Arg Leu Asn Leu Thr Trp Phe Leu Leu Leu Pro  
-20 -15 -10

Pro Gly Gln Cys Arg Ala Val Gly Ala Thr Trp Pro Gly  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 366:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq MVALCCCLWKISG/CE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys Leu Trp Lys  
-15 -10 -5

Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu Leu Lys Cys  
1 5 10

Leu Leu Asp Lys Ala His Val Gly  
15 20

## (2) INFORMATION FOR SEQ ID NO: 367:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq CVCAAXXSQSLX/XX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

```

Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Xaa Xaa
-20 -15 -10

Ser Gln Ser Leu Xaa Xaa Xaa Ala Ala Val Ala Ala Ala Gly Gly Arg
-5 1 5 10

Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu Thr Xaa Ile
15 20 25

Ser Gln Tyr Asp Lys Glu Xaa Gly Xaa Trp Asn Lys Phe Arg Asp Asp
30 35 40

Xaa Tyr
45

```

## (2) INFORMATION FOR SEQ ID NO: 368:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq MVALCCCLWKISG/CE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

```

Met Ser Met Gln Phe Leu Phe Lys Met Val Ala Leu Cys Cys Cys Leu
-20 -15 -10

Trp Lys Ile Ser Gly Cys Glu Glu Val Pro Leu Thr Tyr Asn Leu Leu
-5 1 5 10

Lys Cys Leu Leu Asp Lys Ala His Cys Val Leu Leu Thr Pro Cys Gly

```

15

20

25

Tyr Ile Phe Ser Leu Ile Ser Pro Gly  
30 35

## (2) INFORMATION FOR SEQ ID NO: 369:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq LWILLGSLSCRTS/NR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

Met Ala Gln His Leu Trp Ile Leu Leu Gly Ser Leu Ser Cys Arg Thr  
-15 -10 -5

Ser Asn Arg Arg  
1

## (2) INFORMATION FOR SEQ ID NO: 370:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1  
seq LYLFGSGFWTFXLG/KE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

```

Met Asn Lys Glu Xaa Val Ser Xaa Glu Arg Xaa Ala Gln Val Arg Leu
 -25 -20 -15

Tyr Leu Phe Ser Gly Phe Trp Thr Phe Xaa Leu Gly Lys Phe Lys Gln
 -10 -5 1

Gly Glu Xaa Ser Tyr Xaa Xaa Ile Leu Glu Arg Leu Leu Trp Gln Gln
 5 10 15 20

Gln Tyr Xaa Gly Trp Leu Val Gly Asp Lys Arg
 25 30

```

## (2) INFORMATION FOR SEQ ID NO: 371:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq IVFIFLILLNTAA/QV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

```

Met Val Leu Trp Arg Ala Lys Ile Xaa Arg Asn Val Pro Val Thr Leu
 -50 -45 -40

Ser Glu Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys
 -35 -30 -25

Asn Tyr Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile
 -20 -15 -10

Leu Leu Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp
 -5 1 5 10

Leu Ser Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn
 15 20 25

```

## (2) INFORMATION FOR SEQ ID NO: 372:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -18..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6  
seq FTSVLWLTSPSQP/NT
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Leu Leu Xaa Phe Phe Thr Ser Val Leu Trp Leu Thr Ser Pro Ser  
-15 -10 -5

Gln Pro Asn Thr Cys Pro Ser Ser Leu Leu Cys Thr Tyr Pro Asn Leu  
1 5 10

Asn Pro Pro Trp  
15

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -22..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.9  
seq IILGCLALFLLQ/RK
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

Met Glu Leu Ile Ser Pro Thr Val Ile Ile Ile Leu Gly Cys Leu Ala  
-20 -15 -10

Leu Phe Leu Leu Leu Gln Arg Lys Asn Leu Arg Arg Pro Trp  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq TWLGLLSFQNLHC/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met His Gly Phe Glu Ile Ile Ser Leu Lys Glu Glu Ser Pro Leu Gly  
-45 -40 -35  
Lys Val Ser Gln Gly Pro Leu Phe Asn Val Thr Ser Gly Ser Ser Ser  
-30 -25 -20  
Pro Val Thr Trp Leu Gly Leu Leu Ser Phe Gln Asn Leu His Cys Phe  
-15 -10 -5 1  
Pro Asp Leu Pro Gly  
5

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -56..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq NTLFLHLSGLSAA/DT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Met Thr Trp Val Arg His Ala Pro Gly Lys Ser Leu Glu Trp Val Ala  
-55 -50 -45  
Thr Val Thr Asp Gly Gly Asp Lys Thr Phe Tyr Ala Ala Ser Val Lys

-40                      -35                      -30                      -25  
Gly Arg Phe Asn Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu  
                         -20                      -15                      -10  
                         ..  
His Leu Ser Gly Leu Ser Ala Ala Asp Thr Gly Trp Trp Gly Ile  
                         -5                      1                      5

## (2) INFORMATION FOR SEQ ID NO: 376:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq LTSFFSLTANCQS/AG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

Met Leu Thr Ser Phe Phe Ser Leu Thr Ala Asn Cys Gln Ser Ala Gly  
                         -10                      -5                      1  
Thr Ile Ser Phe Ala Ala Phe Ser Leu Met Pro Gly  
                         5                      10

## (2) INFORMATION FOR SEQ ID NO: 377:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq LTPLEFFMXPTGFS/SP

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

```
Met Leu Leu Cys Leu Leu Thr Pro Leu Phe Phe Met Xaa Pro Thr Gly
 -15 -10 -5

Phe Ser Ser Pro Ser Pro Gly
 1 5
```

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq HSLFLSLLGLCPS/KT

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

```
Met Asp Asp Asp Tyr Glu Ala Tyr His Ser Leu Phe Leu Ser Leu Leu
 -20 -15 -10

Gly Leu Cys Pro Ser Lys Thr Pro Ile Asn Glu Asn Ala Pro Val Phe
 -5 1 5 10

Asp Pro Glu Pro Val
 15
```

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1



(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.7  
 seq WLVWLLLGHMVVS/QM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

Met Glu Trp Gly Lys Gln Trp Leu Val Trp Leu Leu Leu Gly His Met  
                   -15                                  -10                                  -5  
 Val Val Ser Gln Met Ala Thr Leu Leu Ala Arg Lys His Arg Pro Trp  
                   1                                          5                                          10

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -39..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.7  
 seq LTQGVWLWILVIQA/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

Met Arg Arg Gly Lys Arg Leu Leu Glu Ser Gln Ser Ser Ser Pro Lys  
                   -35                                  -30                                  -25  
 Ala Cys Leu Gln Leu Gly Phe Glu Thr Glu Leu Thr Gln Gly Val Leu  
                   -20                                  -15                                  -10  
 Trp Ile Leu Val Ile Gln Ala Val Pro Val Pro Ser Leu Thr Lys Thr  
                   -5                                          1                                          5  
 Lys  
 10

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -20...-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.7  
seq ALLESVVWLPCHG/RG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

Met Val Ala Ala Thr Glu Ala Ala Leu Leu Glu Ser Val Val Trp Leu  
-20 -15 -10 -5  
Pro Cys His Gly Arg Gly Gly Ser  
1

## (2) INFORMATION FOR SEQ ID NO: 382:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19...-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq VSLPLLSSWGSTA/WT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

Met Ser Trp Asn Pro Ser Val Ser Leu Pro Leu Leu Ser Ser Trp Gly  
-15 -10 -5  
Ser Thr Ala Trp Thr Leu  
1

## (2) INFORMATION FOR SEQ ID NO: 383:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -22...-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.6  
seq LILLSLHLERRWT/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

```

Met Lys Arg Ile Gln Gly Ile Leu Phe Leu Ile Leu Leu Ser Leu His
 -20 -15 -10

Leu Glu Arg Arg Trp Thr Ser Pro Ser Asp His Ser Leu Leu Leu Gly
 -5 1 5 10

Gly Asn Ser Leu Ala Gln His Ala Glu Ser Val Val Arg Gln Gly
 15 20 25

```

## (2) INFORMATION FOR SEQ ID NO: 384:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -35...-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.5  
seq LLTFGLEVCLAAG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

```

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
-35 -30 -25 -20

Gln Leu Xaa Leu Xaa Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
 -15 -10 -5

Ala Ala Gly Ser Pro Met Cys Arg Leu Cys Cys Trp Lys Trp
 1 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 385:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq PFALVTSCSSVFS/GD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

Met Ala Ala Gly Val Pro Phe Ala Leu Val Thr Ser Cys Ser Ser Val  
-15 -10 -5

Phe Ser Gly Asp Gln Leu Val Gln His Ile Leu Gly Thr Glu Asp Leu  
1 5 10

Ile Val Glu Val Thr Ser Asn Asp Ala Val Arg Phe Tyr Pro Trp Thr  
15 20 25 30

Ile Asp Asn Lys Tyr Tyr Ser Ala Asp Ile Asn Leu Cys Val Val Pro  
35 40 45

Asn Lys Phe Leu Val Thr Ala Glu Ile Ala Glu Ser Val Gln Ala Phe  
50 55 60

Val Val Tyr Phe Asp Xaa Thr Gln Xaa Ser Gly Leu Asp Ser Val Ser  
65 70 75

Ser Trp Leu Pro Leu Ala Lys Ala Trp Leu Pro Glu Val Met Ile Leu  
80 85 90

Val Cys Asp Arg Val Ser Glu Asp Gly Ile  
95 100

## (2) INFORMATION FOR SEQ ID NO: 386:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
                        seq TVFLXFCFPRCHS/DS
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

Met Thr Val Phe Leu Xaa Phe Cys Phe Pro Arg Cys His Ser Asp Ser
-10 -5 1

His Xaa Xaa Gln Gln Ser Ala
5

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: AMINO ACID
(C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -48..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
 seq ILLEVFVWNGLQG/LP
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

```

Met Xaa Pro Asn Asn Phe Trp Gln Lys Leu Gly Arg Lys Lys Pro Arg
 -45 -40 -35

Ile Phe Thr Cys Thr Gln Ser Ser Thr Gly Glu Ala Ala Val Lys Ala
 -30 -25 -20

Glu Asn Leu Ile Leu Leu Glu Val Phe Val Trp Asn Gly Leu Gln Gly
 -15 -10 -5

Leu Pro Ser Glu Leu Ser Asp Thr Ser Gly Ser Ser Lys Lys Leu Gly
 1 5 10 15

Ser Leu Val Gly Trp Trp Arg Thr Leu Lys Met Ala Pro Ala Cys Leu
 20 25 30

Trp Ser Met Trp Glu Ser Pro Pro Arg
 35 40

```

## (2) INFORMATION FOR SEQ ID NO: 388:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq ALYIMCVPHSVWG/CA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met Phe Arg Ser Asp Arg Met Trp Xaa Cys His Trp Lys Trp Lys Pro  
-35 -30 -25

Ser Pro Leu Leu Phe Leu Phe Ala Leu Tyr Ile Met Cys Val Pro His  
-20 -15 -10 -5

Ser Val Trp Gly Cys Ala Asn Cys Arg Val Val Leu Ser Asn Pro Ser  
1 5 10

Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser Gln  
15 20 25

Ala Cys Met Trp Thr Leu Arg Asp Pro  
30 35

## (2) INFORMATION FOR SEQ ID NO: 389:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq LVALSSELPFLGA/G/

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

```

Met Thr Gln Arg Ser Ile Ala Gly Pro Ile Cys Asn Leu Lys Phe Val
-30 -25 -20

Thr Leu Leu Val Ala Leu Ser Ser Glu Leu Pro Phe Leu Gly Ala Gly
-15 -10 -5 1

Val Gln Leu Gln Asp Asn Gly Tyr Asn Gly Leu Leu Ile Ala Ile Asn
 5 10 15

Pro Gln Val Pro Glu Asn Gln Asn Leu Ile Ser Asn Ile Lys Glu Met
 20 25 30

Ile Thr Glu Ala Ser Phe Tyr Leu Phe Asn Ala Thr Lys Arg Arg Val
 35 40 45

Phe Phe Arg Asn Ile Lys Ile Leu Ile Pro Ala Gln
 50 55 60

```

## (2) INFORMATION FOR SEQ ID NO: 390:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq IIPLLLLLSACN/VH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

```

Met Ile Ile Pro Leu Leu Leu Leu Arg Ser Ala Cys Asn Val His
 -10 -5 1

Leu Pro His Gln Thr Ala Ser Pro Ala Ser Leu Ser Pro Gln Gly Leu
 5 10 15

Ala Trp Gly Leu Leu His Gly Gly Cys Ser Val Thr Val Arg
 20 25 30

```

## (2) INFORMATION FOR SEQ ID NO: 391:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.3  
seq VLLLSXNLNLIQ/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

Met Xaa Ser Pro Leu Pro Val Leu Leu Leu Ser Xaa Asn Leu Asn Leu  
-15 -10 -5

Ile Ile Gln Ser Ser  
1

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -46..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2  
seq LLTFLVFTXKLSS/LN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

Met Leu Met Cys Lys Met Leu Lys Ser Gln Lys Asn Cys Gln Glu Asn  
-45 -40 -35

Xaa Xaa Ile Lys Ile Ile Leu Phe Leu Lys Pro Met Cys Ser Pro Gln  
-30 -25 -20 -15

Tyr Leu Leu Thr Phe Leu Val Phe Thr Xaa Lys Leu Ser Ser Leu Asn  
-10 -5 1

Ile Xaa Lys Phe His  
5



## (2) INFORMATION FOR SEQ ID NO: 393:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -52..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq IIVILHCAASIIS/CP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

Met Lys Lys Lys Ser Ser Pro Asn Gln Tyr Leu His Ser Ser Leu His  
-50 -45 -40

Xaa Ile Arg Leu Phe Ser Phe Leu His Phe Ser Glu Glu Gly Val Leu  
-35 -30 -25

Leu Leu Ala Ile Asp Leu Lys Ile Ile Val Ile Leu His Cys Ala Ala  
-20 -15 -10 -5

Ser Ile Ile Ser Cys Pro Ser  
1

## (2) INFORMATION FOR SEQ ID NO: 394:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq ATSVSLEAQSCFA/WP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

```

Met Phe Ser Cys Phe Phe Ser Thr Ser Leu Ala Thr Ser Val Ser Leu
 -20 -15 -10

Glu Ala Gln Ser Cys Phe Ala Trp Pro Leu Ile Val Ser Phe Pro Gln
 -5 1 5

Gly Ser Leu Leu Ser Pro Phe Leu Leu Met Ser Tyr Asn Leu Ser His
 10 15 20 25

Leu Ile Tyr Ser Gly Glu Leu Asn Gly Arg Leu Tyr Ala Glu Asn Ser
 30 35 40

Gln Ile Cys Ile Cys Ser Pro Ala Gly
 45 50

```

## (2) INFORMATION FOR SEQ ID NO: 395:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -50..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq RTALILAVCCGSA/SI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

```

Met His-His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys
-50 -45 -40 -35

Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala
 -30 -25 -20

Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly
 -15 -10 -5

Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser
 1 5 10

Ser Gln Asp Leu Ser Gly Gln Thr Ala Pro Gly
 15 20 25

```

## (2) INFORMATION FOR SEQ ID NO: 396:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq IYFFACFQALTSS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Ser Pro Cys Ile Tyr Phe Phe Ala Cys Phe Gln Ala Leu Thr Ser  
-15 -10 -5

Ser Ser Pro Pro Gln  
1

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq VSGASGFLPPARS/RI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Met Ala Glu Glu Met Glu Ser Ser Leu Glu Ala Xaa Phe Ser Ser Ser  
-35 -25 -20

Gly Ala Val Ser Gly Ala Ser Gly Phe Leu Pro Pro Ala Arg Ser Arg  
-15 -10 -5 1

Ile Phe Lys Ile Ile Val Ile Gly Asp Xaa Asn Val Gly Lys Thr Cys  
5 10 15

Leu Thr Tyr Arg Phe Cys Ala Gly Arg Phe Pro Asp Arg Thr Glu Ala

20                      25                      30  
 Thr Ile Gly Val Asp Phe Arg Glu Arg Ala Val Glu Ile Asp Gly Glu  
     35                      40                      45  
 Arg Ile Lys Ile Gln Leu Trp Asp Thr Ala  
     50                      55

## (2) INFORMATION FOR SEQ ID NO: 398:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq VSGASGFLPPARS/RI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Ala Glu Glu Met Glu Ser Ser Leu Glu Ala Ser Phe Ser Ser Ser  
     -30                      -25                      -20  
 Gly Ala Val Ser Gly Ala Ser Gly Phe Leu Pro Pro Ala Arg Ser Arg  
     -15                      -10                      -5                      1  
 Ile Phe Lys Ile Ile Val Ile Gly Asp Ser Asn Val Xaa Lys Thr Cys  
                     5                      10                      15  
 Leu Thr Tyr Arg Phe Cys Ala Gly Arg Phe Pro Asp Arg  
     20                      25                      30

## (2) INFORMATION FOR SEQ ID NO: 399:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -27..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5  
 seq HSLILLKPLCLP/NN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Leu Val Leu Gly Ser Pro Leu Leu Gly Pro Leu Leu Trp His Leu  
 -25 -20 -15  
 Ser Leu Ile Leu Leu Lys Pro Leu Cys Leu Pro Asn Asn Leu Pro Leu  
 -10 -5 1 5  
 Ala Leu Gly Arg Cys Leu Cys Leu His Ser  
 10 15

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -55..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5  
 seq VLFMTTAVDLVIT/EV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met His Leu Leu Asp Leu Glu Ser Met Gly Lys Ser Ser Asp Gly Lys  
 -55 -50 -45 -40  
 Ser Tyr Val Ile Thr Gly Ser Trp Asn Pro Lys Ser Pro His Phe Gln  
 -35 -30 -25  
 Val Val Asn Glu Glu Thr Pro Lys Asp Lys Val Leu Phe Met Thr Thr  
 -20 -15 -10  
 Ala Val Asp Leu Val Ile Thr Glu Val Gln Glu Pro Val Arg Phe Leu  
 -5 1 5  
 Leu Glu Thr Lys Val Arg Val Cys Ser Pro Asn Glu Arg Leu Phe Trp  
 10 15 20 25  
 Pro Ala

## (2) INFORMATION FOR SEQ ID NO: 401:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq VLFVFSSIPLTFL/FQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Glu Asn Leu Lys Asp Phe Tyr Val Leu Phe Val Phe Ser Ser Ile  
-20 -15 -10

Pro Leu Thr Phe Leu Phe Gln Lys Leu Pro Phe Val Trp Ile Xaa Glu  
-5 1 5 10

Glu Thr Leu Glu Thr Trp Tyr Leu Lys Ser Trp  
15 20

## (2) INFORMATION FOR SEQ ID NO: 402:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq LSIFSLVLPVCRM/HR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Met Pro Gln Tyr Cys Leu Ser Ile Phe Ser Leu Val Leu Pro Val Cys  
-15 -10 -5

Arg Met His Arg

1

## (2) INFORMATION FOR SEQ ID NO: 403:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq LLAFGTSCSVVLY/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

Met Val Ala Pro Val Leu Glu Thr Ser His Val Phe Cys Cys Pro Asn  
-40 -35 -30

Arg Val Arg Gly Val Leu Asn Trp Ser Ser Gly Pro Arg Gly Leu Leu  
-25 -20 -15

Ala Phe Gly Thr Ser Cys Ser Val Val Leu Tyr Asp Pro Leu Gly Cys  
-10 -5 1 5

Cys Tyr Gln Leu Glu Trp Ser His Arg Pro Phe Arg  
10 15

## (2) INFORMATION FOR SEQ ID NO: 404:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq LSWLITWFGHXLS/DF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

```

Met Pro Ile Ile Asp Gln Val Asn Pro Glu Leu His Asp Phe Met Gln
 -35 -30 -25

Ser Ala Gln Val Gly Thr Ile Phe Ala Leu Ser Trp Leu Ile Thr Trp
 -20 -15 -10

Phe Gly His Xaa Leu Ser Asp Phe Arg His Val Val Arg Leu Tyr Asp
 -5 1 5 10

Phe Phe Leu Ala Cys His Pro Leu Met Pro Ile Tyr Phe Ala Ala Val
 15 20 25

Ile Val Leu Tyr Arg Glu Gln
 30

```

## (2) INFORMATION FOR SEQ ID NO: 405:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq GLCVLVPCSXSXX/WR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

```

Met Glu Thr Xaa Cys Pro Cys Cys Cys Cys Pro Cys Xaa Gly Xaa Gly
 -45 -40 -35

Ser Leu Xaa Xaa Lys Pro Val Tyr Glu Leu Gln Val Gln Lys Ser Val
 -30 -25 -20

Thr Val Gln Glu Gly Leu Cys Val Leu Val Pro Cys Ser Xaa Ser Xaa
 -15 -10 -5

Xaa Trp Arg Ser Trp Tyr Ser Ser Pro Pro Leu Tyr Val Tyr Trp Phe
 1 5 10 15

Arg Asp Gly Glu Ile Pro Tyr Tyr Ala Glu Val Val Ala Thr Asn Asn
 20 25 30

Pro Asp Arg Arg Xaa Lys Xaa Xaa Xaa Xaa Xaa Pro Ile Pro Pro Pro
 35 40 45

```



Trp Gly Cys Pro Glu Glu Glu Leu  
50 55

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq IYFFACFXLTSS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

Met Ser Pro Cys Ile Tyr Phe Phe Ala Cys Phe Xaa Xaa Leu Thr Ser  
-15 -10 -5  
Ser Ser Pro Pro His Pro Cys Pro Lys Cys Trp Pro Ser Ser Gly Ser  
1 5 10 15  
Ile Pro Leu

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq VLKCLSFSXPSLP/GF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

(21) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -69..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.6  
seq LGPSLSSLPSALS/LM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

```

Met His His Arg Met Asn Glu Met Asn Leu Ser Pro Val Gly Met Glu
 -65 -60 -55

Gln Leu Thr Ser Ser Ser Val Ser Asn Ala Leu Pro Val Ser Gly Ser
 -50 -45 -40

His Leu Gly Leu Ala Ala Ser Pro Thr His Ser Ala Ile Pro Ala Pro
 -35 -30 -25

Gly Leu Pro Val Ala Ile Pro Asn Leu Gly Pro Ser Leu Ser Ser Leu
 -20 -15 -10

Pro Ser Ala Leu Ser Leu Met Leu Pro Met Gly Xaa Gly Asp Arg Gly
 -5 1 5 10

Val Met Cys Gly Leu
 15

```

## (2) INFORMATION FOR SEQ ID NO: 410:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.6  
seq IWNLFSLFSTST/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

```

Met Leu His Ser Asp Asn Ile Trp Asn Leu Phe Ser Leu Phe Ser Thr
 -15 -10 -5

```

Ser Thr Thr Leu Pro Arg  
1

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq FHSAAGWSGGGQA/CG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Gln Pro Ala Ser Pro Pro Ala Arg Trp Ser Phe His Ser Ala Ala  
-20 -15 -10  
Gly Trp Ser Gly Gly Gly Gln Ala Cys Gly Gly His Ser Cys Asp Gln  
-5 1 5  
Val Leu Ala Val Ile Glu Leu Leu Asn Pro Leu Arg  
10 15 20

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq LLAGSISHMFSQA/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Cys Phe Ser Phe Leu Leu Ala Gly Ser Ile Ser His Met Phe Ser  
-15 -10 -5

Gln Ala Leu Pro Leu His Ser Pro Gly Leu Pro Thr Thr Asn Arg Thr  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 413:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Prostate

(2X) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
                        seq SILFHCSVCLFLC/QY
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Met Tyr Gly Phe Ile Ile Gly Leu Ser Ile Leu Phe His Cys Ser Val
-20 -15 -10

Cys Leu Phe Leu Cys Gln Tyr His Ala Trp
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq SLLGCXLA^{IN}INT/FP

(kt) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Ser Phe Gly Xaa Ile Leu Thr Phe Arg Val Ser Leu Leu Gly Cys
 -20 -15 -10

Xaa Leu Ala Ile Asn Ile Asn Thr Phe Pro Ser Asn Asn His Leu
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq LGRLCAGSSGVXG/AR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu Cys Ala Gly
 -20 -15 -10

Ser Ser Gly Val Xaa Gly Ala Arg Ala Xaa Leu Ser Arg Ser Trp Gln
 -5 1 5 10

Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Ser Ser Arg Glu Val Asp
 15 20 25

Arg Met Val Ser Thr Pro Ile Gly Gly Leu Ser Tyr Val Gln Gly Cys
 30 35 40

Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly Gln Cys Leu Glu Thr
 45 50 55

Thr Ala Gln Arg Val Pro
 60

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -23..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq LVSIFFFW EVTNA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

Met Phe Asn Thr Ile Tyr Leu Val Ile Ser Leu Val Ser Ile Phe Phe
-20 -15 -10
Phe Trp Glu Val Thr Asn Ala Phe Leu Lys Ala Arg Arg Trp
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -22..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq SLPLTTGSSWSLS/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Ala Leu Pro Pro Lys Gly Cys Gly Ser Leu Pro Leu Thr Thr Gly
-20 -15 -10
Ser Ser Trp Ser Leu Ser Ser Gln Ile Gly Ser Pro Ala Ile Ser Asn
-5 1 5 10
Pro Arg

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -16..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3
seq FLSWASFLAPLLR/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

Met Phe Val Phe Leu Ser Trp Ala Ser Phe Leu Ala Pro Leu Leu Arg
-15 -10 -5

Ser Pro Phe Leu His Cys Leu Met Gly Met Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -28..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.3
seq LLSCSPLXPLGKS/GF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

Met Xaa Met Lys Ser Ala Asn Lys Ile Thr Leu Leu Xaa His His Leu
-25 -20 -15

Leu Ser Cys Ser Pro Leu Xaa Pro Leu Gly Lys Ser Gly Phe Ser Ser
-10 -5 1

Cys Gln Arg Leu Gly Lys Arg Ala Leu Val Phe Pro Ile Xaa Lys Xaa
5 10 15 20

Ile Ile Thr

(2) INFORMATION FOR SEQ ID NO: 420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SFLLLFIVIPQTP/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

Met Cys Asn Tyr Asn Ile Tyr Val Leu Tyr Asn Ile Gly Tyr Leu Tyr
-30 -25 -20

His Pro Lys Ser Phe Leu Leu Leu Phe Ile Val Ile Pro Gln Thr Pro
-15 -10 -5

Arg Pro
1

(2) INFORMATION FOR SEQ ID NO: 421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq PLLAAPLLRSLLP/RX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

Met Ala Val Ala Met Val Lys Leu Cys Glu Arg Ala Gly Leu Pro Leu
-25 -20 -15

Leu Ala Ala Pro Leu Leu Arg Ser Leu Leu Pro Arg Xaa Pro Gln Pro
 -10 -5 1 5
 Gly Pro Ala Gln Pro Arg Ser Val Gln Gly Gln Arg Cys Pro Ala Arg
 10 15 20
 His Pro Pro Gly Asn Leu Val Cys Glu Arg Gly Ala Xaa Val Asn Gly
 25 30 35
 Val Thr Ala Gly Ala Xaa Gly Xaa Leu Arg Gly Leu His Arg Gly Xaa
 40 45 50
 Arg Ala Leu Gly Cys Ser Ala His Arg Pro Xaa His Ser Ala Arg Val
 55 60 65
 Arg Pro Pro Ala
 70

(2) INFORMATION FOR SEQ ID NO: 422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -122..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq DVLGLLKDVLLA/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

Met Leu Asn Val Val Arg Ala Leu Arg Xaa Pro Gln Trp Cys Ala Glu
 -120 -115 -110
 Tyr Cys Leu Ser Ile His Tyr Gln His Gly Gly Val Ile Cys Thr Gln
 -105 -100 -95
 Val His Lys Gln Thr Val Val Gln Leu Ala Leu Arg Val Ala Asp Glu
 -90 -85 -80 -75
 Met Asp Val Asn Ile Gly His Glu Val Gly Tyr Val Ile Pro Phe Glu
 -70 -65 -60
 Asn Cys Cys Thr Asn Glu Thr Ile Leu Arg Tyr Cys Thr Asp Asp Met
 -55 -50 -45
 Leu Gln Arg Glu Met Met Ser Asn Pro Phe Leu Gly Ser Tyr Gly Val
 -40 -35 -30

Ile Ile Leu Asp Asp Ile His Glu Arg Ser Ile Ala Thr Asp Val Leu
-25 -20 -15
Leu Gly Leu Leu Lys Asp Val Leu Leu Ala Arg Pro Glu Leu Lys
-10 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -2/-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq AGLCIGSTSYVHG/DI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

Met His Ala Gly Leu Glu Arg Xaa Ser Xaa Gln Lys Ala Leu Ala Gly
-25 -20 -15
Leu Cys Ile Gly Ser Thr Ser Tyr Val His Gly Asp Ile Leu Arg Thr
-10 -5 1 5
Glu Arg

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35/-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq LLGSLSLWRWSAM/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

```

Met Leu Asn Gly Pro Phe Gln His Arg Asn Ser Arg Ile Met Thr His
-35          *   -30          -25          -20

Arg Ser Ala Glu Lys Thr Leu Leu Gly Ser Leu Ser Leu Trp Arg Trp
          -15          -10          -5

Ser Ala Met Glu Pro Thr Asp Arg Cys Thr Arg Val Gly
      1              5              10

```

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq IAVGLTCQHVSHA/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

```

Met Arg Val Lys Asp Pro Thr Lys Ala Leu Pro Glu Lys Ala Lys Arg
          -40          -35          -30

Ser Lys Arg Pro Thr Val Pro His Asp Glu Asp Ser Ser Asp Asp Ile
          -25          -20          -15

Ala Val Gly Leu Thr Cys Gln His Val Ser His Ala Ile Ser Val Asn
          -10          -5              1

His Val Lys Arg Ala Ile Ala Glu Asn Leu Trp Ser Val Cys Ser Glu
      5              10              15              20

Cys Leu Lys Glu Arg Arg Phe Tyr Asp Gly Gln Leu Val Leu Thr Ser
          25              30              35

Asp Ile Trp Leu Cys Leu Lys Cys Gly Phe Gln Gly Cys Gly Lys Asn
          40              45              50

Ser Glu Ser Gln His Ser Leu Lys His Phe Lys Ser Ser Arg Thr Glu
          55              60              65

Pro His Cys Ile Ile Ile Asn Leu Ser Thr
      70              75

```

(2) INFORMATION FOR SEQ ID NO: 426:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
(B) TYPE: AMINO ACID
(C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(1x) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -28..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
 seq FSLALLSMLKGTG/KV
```

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Pro Gln Lys Gly Leu Gly Leu Leu Gly Ile Leu Ser Gly Asp Phe  
-25 -20 -15

Ser Leu Leu Ala Leu Ser Met Leu Lys Gly Thr Gly Lys Val Gly Gly  
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -55..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
                        seq AALCGISLSQLFP/EP
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

Met Ala Met Trp Asn Arg Pro Xaa Xaa Xaa Leu Pro Gln Gln Pro Leu
-55 -50 -45 -40

Xaa Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg
-35 -30 -25

Xaa Xaa Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile
-20 -15 -10
Ser Leu Ser Gln Leu Phe Pro Glu Pro Glu His Ser Ser Phe Cys Thr
-5 1 5
Glu Phe Met Ala Gly Leu Val Xaa Trp Leu Glu Leu Ser Glu Ala Val
10 15 20 25
Leu Pro Thr Met Thr Ala
30

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq LLLSPWVTVPWWS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Leu Cys Phe Gly Asp Leu Leu Leu Ser Pro Trp Val Thr Val Pro
-15 -10 -5
Val Trp Ser Ser Ser Pro Trp
1

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -27..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq LIYFLGLAADTYF/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

Met Gln Glu Asn Ala His Asn Leu Arg Leu Phe Lys Cys Leu Leu Ile
 -25 -20 -15
 Tyr Phe Leu Gly Leu Ala Ala Asp Thr Tyr Phe Arg Ser Lys Arg Lys
 -10 -5 1 5
 Pro Val Ser Phe Val Val Thr Val Xaa Xaa Gly Xaa Tyr Ala Thr Gly
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -59..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq SVATALFPPLCIS/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

Met His Thr Cys Ser Leu Pro Cys Leu Leu Phe Ala Gln Leu Leu Glu
 -55 -50 -45
 Phe Cys Ser Phe Pro Pro Asp Val Pro His Asn Cys Ala Pro Ile Val
 -40 -35 -30
 Ser Val Arg Pro Pro Asn Ile Val Ala Ala Phe Glu Gly Cys Ser Val
 -25 -20 -15
 Ala Thr Ala Leu Phe Pro Pro Leu Cys Ile Ser Thr Gly Asn Glu
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids
 (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -28..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4
seq PLLGVLEFFQGVYI/VF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

```
Met Gln Gln Arg Gly Ala Ala Gly Ser Arg Gly Cys Ala Leu Phe Pro
      -25                -20                -15

Leu Leu Gly Val Leu Phe Phe Gln Gly Val Tyr Ile Val Phe Ser Leu
      -10                -5                1

Glu Ile Arg Ala Asp Ala His Val Arg Gly Tyr Val Gly Glu Lys Ile
      5                10                15                20

Lys Leu Lys Cys Thr Phe Lys Ser Thr Ser Asp Val Thr Asp Lys Leu
      25                30                35

Thr Ile Asp Trp Thr Tyr Arg Pro Pro Ser Ser Ser His Thr Val Ser
      40                45                50

Ile Xaa His Tyr Gln Ser Phe Gln Tyr Pro Thr Thr Ala Gly Thr Phe
      55                60                65
```

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -39..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.9
seq LILNRSLEPTASSS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:


```

Met Xaa Xaa Ser Ile Phe Ile Ser Glu Lys Tyr Gly Leu Cys Pro Ser
      -35          -30          -25

Lys Thr Pro Ile Met Lys Met Leu Pro Ser Leu Ile Leu Asn Arg Ser
      -20          -15          -10

Leu Pro Thr Ala Ser Ser Ser Ser Ser Arg Lys Asp Phe Arg Leu Pro
      -5              1              5

Gln Thr Arg Arg Arg Ile Ile Met Val Pro Arg Lys Glu Asp Gln Thr
      10              15              20              25

Pro Leu Asn Pro Ala Ser Gln Pro Gln Ala Pro Pro Lys Pro Ile Pro
      30              35              40

Ser Xaa Lys Ser Leu Glu Ala Xaa Asp Xaa Xaa Xaa Ser Gln Arg Thr
      45              50              55

Xaa Arg Pro Gly Leu Ser Arg Gly Arg Ser Cys
      60              65

```

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq FFVVVLFSGCKV/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

```

Met Ala Phe Asp Val Ser Cys Phe Phe Trp Val Val Leu Phe Ser Ala
-20          -15          -10          -5

Gly Cys Lys Val Ile Thr Ser Trp Asp Gln Met Tyr Ile Glu Lys Glu
      1              5              10

Ala Asn Lys Thr Tyr Asn Cys Glu Asn Leu Gly Leu Ser Glu Ile Pro
      15              20              25

Asp Thr Leu Pro Asn Thr Thr Glu Phe Leu Glu Phe Ser Phe Asn Phe
      30              35              40

Leu Pro Thr Ile His Asn Arg Thr Ser Ser Arg
      45              50              55

```

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -96..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq IMNLTVMMLDTAXG/KX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

```

Met Glu Val Ala Ala Asn Cys Ser Leu Arg Val Lys Arg Pro Leu Leu
  -95                      -90                      -85

Asp Pro Arg Phe Glu Gly Tyr Lys Xaa Ser Leu Glu Pro Leu Pro Cys
-80                      -75                      -70                      -65

Tyr Gln Leu Glu Leu Asp Ala Ala Val Ala Xaa Val Lys Leu Arg Asp
          -60                      -55                      -50

Asp Gln Tyr Thr Leu Glu His Met His Ala Phe Gly Met Tyr Asn Tyr
          -45                      -40                      -35

Leu His Cys Asp Ser Trp Tyr Gln Asp Ser Val Tyr Tyr Ile Asp Thr
          -30                      -25                      -20

Leu Gly Arg Ile Met Asn Leu Thr Val Met Leu Asp Thr Ala Xaa Gly
          -15                      -10                      -5

Lys Xaa Arg Glu Val Phe Arg Leu Leu
  1                      5

```

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -39..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq VLAIGLLHIVLLS/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

```

Met Asn Val Gly Thr Ala His Xaa Xaa Val Asn Pro Asn Thr Arg Val
      -35                      -30                      -25

Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu
      -20                      -15                      -10

Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val
      -5                      1                      5

Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu
      10                      15                      20                      25

His Thr Val Lys Gly Xaa Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
      30                      35                      40

Arg Leu Leu Xaa His Xaa Xaa Ala Asp Gly Leu Trp Gly Pro Val
      45                      50                      55
  
```

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -23..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq SWWTLLSSSPSFM/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

```

Met Glu Asn Phe Asn Met Tyr Lys Asn Lys Ser Trp Trp Thr Leu Leu
      -20                      -15                      -10

Ser Ser Ser Pro Ser Phe Met Ile Ser Phe Val Ser Ser Val Leu Pro
      -5                      1                      5

Val Leu Leu Thr Ile Ser Arg Phe Ile Leu Lys Gln Ile Pro Asp Gln
      10                      15                      20                      25
  
```

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq VLAIGLLHIVLLS/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

```

Met Asn Val Gly Thr Xaa His Ser Glu Val Asn Pro Asn Thr Arg Val
      -35                      -30                      -25

Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu
      -20                      -15                      -10

Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val
      -5                      1                      5

Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu
      10                      15                      20                      25

Tyr Thr Val Lys Gly Thr
      30

```

(2) INFORMATION FOR SEQ ID NO: 438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8

seq AAASAVSVLLVAA/ER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

Met Ala Ala Ala Ser Ala Val Ser Val Leu Leu Val Ala Ala Glu Arg
 -10 -5 1

Asn Arg Trp His Arg Leu Pro Ser Leu Leu Leu Pro Pro Arg Thr Trp
 5 10 15

Val Trp Arg Gln Arg Thr Met Lys Tyr Thr Thr Ala Thr Gly Arg Asn
 20 25 30

Met
 35

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
 seq SGSGLSWARLSQS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

Met Ala Tyr Ser Lys Ala Ser Gly Ser Pro Val Leu Ser Gln Ala Val
 -40 -35 -30

Pro Gly Glu Asn Ala Ser His Arg Arg Gly Ser Ala Asp Leu Gly Ser
 -25 -20 -15

Gly Ser Gly Leu Ser Trp Ala Arg Leu Ser Gln Ser Arg Ser Glu Ile
 -10 -5 1

His Ser Ala Gly Pro Pro His Leu Gly Gly Arg Thr Asn Gly Pro Glu
 5 10 15 20

Phe Pro Ala Leu Ser Tyr Ser Ser Gln Leu Leu Ser Leu Ala Gln Leu
 25 30 35

Arg Gly Arg Gly Ile Thr Glu Val Ser Glu Lys Ser Pro Leu Ile
 40 45 50

(2) INFORMATION FOR SEQ ID NO: 440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq RPVLLHLHQTAHA/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

```

Met Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp
  -35                      -30                      -25

Thr Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His
  -20                      -15                      -10

Gln Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His
  -5                      1                      5                      10

Thr Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala
      15                      20                      25

Ile Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile
      30                      35                      40

His Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Gln
      45                      50                      55

```

(2) INFORMATION FOR SEQ ID NO: 441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.7
seq IPCAHMLVCPTIG/DI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

```
Met Ile Ile Cys Tyr Asp Ile Pro Cys Ala His Met Leu Val Cys Pro
      -15                -10                -5
Thr Ile Gly Asp Ile Lys Phe Asp His Leu Met Lys Trp Tyr Pro Ser
      1                5                10
Asp Phe Ser Thr Glu Arg Leu
      15                20
```

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids
(B) TYPE: AMINO ACID
(C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq STLASVPPAATFG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

```
Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val Pro Pro Ala Ala
      -15                -10                -5
Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln Met
      1                5                10
Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro Gln
      15                20                25
Phe Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val Glu
      30                35                40                45
Lys Asn Lys Tyr Asp Ala
      50
```

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -65..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq QLEGLNWLRFSA/QG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Met Gly Glu Asp Pro Xaa Gln Pro Arg Lys Tyr Lys Lys Xaa Lys Xaa
-65 -60 -55 -50
Glu Leu Gln Gly Asp Xaa Pro Pro Ser Ser Pro Thr Asn Asp Pro Thr
-45 -40 -35
Val Lys Tyr Glu Thr Gln Pro Arg Phe Ile Thr Ala Thr Gly Gly Thr
-30 -25 -20
Leu His Met Tyr Gln Leu Glu Gly Leu Asn Trp Leu Arg Phe Ser Trp
-15 -10 -5
Ala Gln Gly Thr Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -42..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq LLGCLQCCWLQSG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met Phe Tyr Val Ala Met Thr Lys Thr His Lys Arg Ile Arg Ser Leu
-40 -35 -30

Cys Asn Ile His His Gly Leu Phe Gln Phe Thr Gln Gln Leu Leu Gly
 -25 -20 -15

Cys Leu Gln Cys Cys Trp Leu Gln Ser Gly Arg Ala Pro Ala Thr Tyr
 -10 -5 1 5

Tyr Leu Val Glu Ser Ile Glu Lys Ser Ala His Gly Ser Val Leu Xaa
 10 15 20

Thr Tyr Asp Gln Thr Gln Thr Arg Ile Gly Arg
 25 30

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq XTCASXNPSQCLA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

Met Val Ser Pro Lys Asp Leu Pro Leu Val Leu Leu Gln Asp Ile Lys
 -60 -55 -50 -45

Val Pro Ser Ser Met Thr Gly Ser His Ala Gly Asn Pro His Ile Glu
 -40 -35 -30

Arg Asn Asp Leu Pro Arg His Gly Ser Pro Gln Phe Phe Thr Gly Xaa
 -25 -20 -15

Thr Cys Ala Ser Xaa Asn Pro Ser Gln Cys Leu Ala Ala Phe
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq FXSLFCLYFSCFL/HI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

Met Glu Phe Xaa Ser Leu Phe Cys Leu Tyr Phe Ser Cys Phe Leu His
-15 -10 -5 1

Ile Ile Tyr Phe Xaa Ser Cys Phe Leu Tyr
 5 10

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -45..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq ALLELIDSPECLS/KC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

Met Ala Leu His Phe Gln Ser Leu Ala Glu Leu Glu Xaa Leu Cys Thr
-45 -40 -35 -30

His Leu Tyr Ile Gly Thr Asp Leu Thr Gln Arg Ile Glu Ala Glu Lys
 -25 -20 -15

Ala Leu Leu Glu Leu Ile Asp Ser Pro Glu Cys Leu Ser Lys Cys Gln
 -10 -5 1

Leu Leu Leu Glu Gln Gly Thr Thr Ser Tyr Ala Gln Leu Leu Ala Ala
 5 10 15

Thr Xaa
20

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq LLLLLITPSPSP/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

Met Arg Thr Leu Phe Gly Ala Val Arg Ala Pro Phe Ser Ser Leu Thr
-25 -20 -15
Leu Leu Leu Ile Thr Pro Ser Pro Ser Pro Leu Leu Phe Asp Arg Gly
-10 -5 1 5
Leu Ser Leu Arg Ser Ala Met Ser
10

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq AVSSLIAVGTSHG/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

Met Arg His Ser Leu Leu Lys Gly Ile Ser Ala Gln Ile Val Ser Ala
-40 -35 -30

Ala Asp Lys Val Asp Ala Gly Leu Pro Thr Ala Ile Ala Val Ser Ser
-25 -20 -15 -10
Leu Ile Ala Val Gly Thr Ser His Gly Leu Ala Gly
-5 1

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LSCFIFFYISSLC/CF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

Met Thr Leu Ser Cys Phe Ile Phe Phe Tyr Ile Ser Ser Leu Cys Cys
-15 -10 -5 1
Phe Leu Ser Tyr Pro Thr Arg
5

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LCFLLPPhRLQEA/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

Met Ile Leu Cys Phe Leu Leu Pro His His Arg Leu Gln Glu Ala Arg
 -15 -10 -5 1

Gln Ile Gln Val Leu Lys Met Leu Pro Arg Glu Lys Leu Arg Arg Arg
 5 10 15

Arg Arg Glu Lys Thr Asn Lys Trp Glu Lys Arg Lys Gly Ser Gly
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq FSLFALNMPLGFC/VY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

Met Phe Ser Leu Phe Ala Leu Asn Met Pro Leu Gly Phe Cys Val Tyr
 -10 -5 1

Val Ile Phe Lys Ile His Asp Trp
 5 10

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5

seq SVWGVLPSPACSA/DL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

```

Met Ala Ser Ser Pro Gly Val Ala Met His Ser Leu Trp Ala Thr Ile
-30          -25          -20

His Thr Ser Val Trp Gly Val Leu Pro Pro Pro Ala Cys Ser Ala Asp
-15          -10          -5          1

Leu Leu Phe Ser Asn Ala Cys Leu Leu Pro His Glu Ile His Leu
      5          10          15

```

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -45..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LPRLLSLSQHSSES/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

```

Met Ser Gln Glu Gly Ala Val Pro Ala Ser Ala Val Pro Leu Glu Glu
-45          -40          -35          -30

Leu Ser Ser Trp Pro Glu Glu Leu Cys Arg Arg Glu Leu Pro Ser Val
      -25          -20          -15

Leu Pro Arg Leu Leu Ser Leu Ser Gln His Ser Glu Ser Trp Ile Glu
      -10          -5          1

His Ile Gln Ile Leu Lys Ile Ile Val Glu Met Phe Leu Pro His Met
      5          10          15

Asn His Leu Thr Leu Glu Gln Thr Phe Phe Ser Gln Val Leu Pro Lys
      20          25          30          35

Thr Val Lys Leu Phe Asp
      40

```

(2) INFORMATION FOR SEQ ID NO: 455:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Cancerous prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -36..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq AAVVFAVVLSIHA/TV
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

Met Thr Arg Glu Cys Pro Ser Pro Ala Pro Gly Pro Gly Ala Pro Leu
 -35 -30 -25

Ser Gly Ser Val Leu Ala Glu Ala Ala Val Val Phe Ala Val Val Leu
 -20 -15 -10 -5

Ser Ile His Ala Thr Val Trp
 1

(2) INFORMATION FOR SEQ ID NO: 456:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -18..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 14.8
 seq LLWWALLLGLAQA/CP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Gln Glu Leu His Leu Leu Trp Trp Ala Leu Leu Leu Gly Leu Ala
 -15 -10 -5

Gln Ala Cys Pro Glu Pro Cys Asp Cys Gly Glu Lys Tyr Gly Phe Gln
 1 5 10

Ile Ala Asp Cys Ala Tyr Arg Asp Leu Glu Ser Val Pro Pro Gly Phe
 15 20 25 30
 Pro Ala Asn Val Thr Thr Leu Ser Leu Ser Ala Asn Arg Leu Pro Gly
 35 40 45
 Leu Pro Glu Gly Ala Phe Arg Glu Val Pro Leu Leu Gln Ser Leu Trp
 50 55 60
 Leu Ala His Asn Glu
 65

(2) INFORMATION FOR SEQ ID NO: 457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.6
seq LLLALCATGAQG/LY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

Met Gly Arg Gln Ala Leu Leu Leu Leu Ala Leu Cys Ala Thr Gly Ala
 -15 -10 -5
 Gln Gly Leu Tyr Phe His Ile Gly Glu Thr Glu Lys Arg Cys Phe Ile
 1 5 10
 Glu Glu Ile Pro Asp Glu Thr Met Val Ile Gly Asn Tyr Arg Thr Gln
 15 20 25 30
 Met Trp Asp Lys Gln Lys Glu Val Phe Leu Pro Ser Thr Pro Gly Leu
 35 40 45
 Gly Met His Val Glu Val Lys Asp Pro Asp Gly Lys Val Val Leu Ser
 50 55 60
 Arg Gln Tyr Gly Ser Glu Gly Arg Phe Thr Phe Thr Ser His Xaa Xaa
 65 70 75
 Gly Asp His Gln Ile Cys Leu His Cys Gly
 80 85

(2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 12.7
seq ILFLLSWGPIQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser
-20 -15 -10

Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg
-5 1 5 10

Arg Leu Ala Ala Leu Glu Glu Arg
15

(2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(E) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -27..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.8
seq LLLLCPLSRGCCP/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Ser Cys Arg Glu Leu Thr His Arg Pro Cys Ser Pro His Leu Leu
-25 -20 -15

Leu Leu Cys Pro Leu Ser Arg Gly Cys Cys Pro Leu Leu Ser Xaa
-10 -5 1 5

Pro Leu Xaa Gly Val Asn Leu Glu Ser Ile Leu Ser Leu Thr Leu Pro
 10 15 20

Pro Ser Pro Ser Ser Val Gly Leu Ser Pro Ser Val Thr Xaa Leu Thr
 25 30 35

Thr Ser Pro Val Ser Leu His Phe Ala Ser Xaa Leu Ala Gly
 40 45 50

(2) INFORMATION FOR SEQ ID NO: 460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5
seq AALLLGLMMVVTG/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
 -20 -15 -10

Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
 -5 1 5 10

Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
 15 20 25

Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
 30 35 40

Xaa Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
 45 50 55

Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
 60 65 70

Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
 75 80 85 90

Trp Leu Val Thr Asp Ile Lys Gly Ala
 95

(2) INFORMATION FOR SEQ ID NO: 461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3
seq VHLLSLCSGKVYA/RM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser
 -20 -15 -10
Leu Cys Ser Gly Lys Val Tyr Ala Arg Met Ala Ser Leu Arg Gly Leu
 -5 1 5
Gly

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LIFLCGAALLAVG/IW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 -25 -20 -15
Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
 -10 -5 1

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
 5 10 15

Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
 20 25 30 35

Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
 40 45 50

Glu Ser Lys Cys Ala Leu Val Thr Phe
 55 60

(2) INFORMATION FOR SEQ ID NO: 463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq IVSLLGFVATVTL/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

Met Trp Ala Phe Ser Glu Leu Pro Met Pro Leu Leu Ile Asn Leu Ile
 -25 -20 -15

Val Ser Leu Leu Gly Phe Val Ala Thr Val Thr Leu Ile Pro Ala Phe
 -10 -5 1

Arg Gly His Phe Ile Ala Ala Arg Leu Cys Gly Gln Asp Leu Asn Lys
 5 10 15 20

Thr Ser Gln

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq VLMRLVASAYSIA/OK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

Met Ala Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr
-15 -10 -5

Ser Ile Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu
1 5 10

Gly Asp Leu Gly Ile Val Glu Xaa Thr Cys Ala Thr Asp Leu Gln Thr
15 20 25

Lys Ala Asp Arg Leu Ala Gln Met Xaa Ile Cys Ser Ser Leu Ala Arg
30 35 40 45

Lys Phe Pro Lys Leu Thr Ile Ile Gly Glu Glu Asp Leu Pro Ser Xaa
50 55 60

Glu Val Asp Gln Glu
65

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq VHLLSLCSGKAIC/KN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

```
Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser
      -20                      -15                      -10

Leu Cys Ser Gly Lys Ala Ile Cys Lys Asn Gly Ile Ser Lys Arg Thr
      -5                      1                      5
```

Phe Glu Glu Ile Lys Glu Glu Ile Ala Ser Cys Gly Asp Val Ala Lys
 10 15 20
 Ala Ile Ile Asn Leu Ala Val Tyr Gly Lys Ala Gln Asn Arg Ser Tyr
 25 30 35 40
 Xaa Arg Leu Ala Leu Leu Val
 45

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq ALXVLP LLGLHEA/AS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Met Ala Asp Thr Thr Pro Asn Gly Pro Gln Gly Ala Gly Ala Val Gln
 -50 -45 -40
 Phe Met Met Thr Asn Lys Leu Asp Thr Ala Met Trp Leu Ser Arg Leu
 -35 -30 -25 -20
 Phe Thr Val Tyr Cys Ser Ala Leu Xaa Val Leu Pro Leu Leu Gly Leu
 -15 -10 -5
 His Glu Ala Ala Ser Phe Tyr Gln Arg Ala Leu Leu Ala Asn Ala Leu
 1 5 10
 Thr Ser Ala Leu Arg Leu His Gln Arg Leu Pro His Phe Gln Leu Ser
 15 20 25
 Arg Ala Phe Leu Ala Gln Ala Leu Leu Glu Asp Ser Cys His Tyr Leu
 30 35 40 45
 Leu Tyr Ser Leu Ile Phe Val Asn Ser Tyr Pro Val Thr Met Ser Ile
 50 55 60
 Phe Pro Val Leu Leu Phe
 65

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq XVLVLSVVXXAMA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

```

Met Arg Phe Arg His Phe Xaa Lys Xaa Ile Gly Xaa Val Leu Val Leu
      -20                      -15                      -10

Ser Val Val Xaa Xaa Ala Met Ala Ala Phe Ala Val Xaa Pro Gln Gly
      -5                      1                      5

Pro Ala Leu Xaa Ser Glu Pro Xaa Xaa Xaa Gly Ser Pro Thr Ser Pro
      10                      15                      20

Lys Pro Gly Val Asn Ala Gln Phe Leu Pro Gly Phe Leu Met Gly Xaa
      25                      30                      35                      40

Leu Pro Ala Pro Val Thr Pro Gln Pro
      45

```

(2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(12) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -40..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.2
seq LCVVFASVASCDAAV

(11) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

```

Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu
-40                -35                -30                -25

Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Val Glu Phe
                -20                -15                -10

Ala Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala
                -5                1                5

Glu Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro
10                15                20

Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Glu Thr Ile Ser Glu
25                30                35                40

Pro Lys Thr Tyr Val Asp Leu Thr Asn Glu Glu Thr Thr Asp Ser Thr
                45                50                55

Thr Ser Lys Ile Ser Pro Ser Glu Asp Thr Gln Gln Glu Asn Gly Ser
                60                65                70

Met Phe Ser Leu Ile Thr Trp Asn Ile Asp Gly Leu Asp Leu Asn Asn
75                80                85

Leu Ser Glu Arg Ala Arg Gly Val Cys Ser Tyr Leu Ala Leu Tyr Ser
90                95                100

Pro Asp Val Ile Phe Leu Gln Glu Val Ile Pro Pro Tyr Tyr Ser Tyr
105                110                115                120

Leu

```

(2) INFORMATION FOR SEQ ID NO: 469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -122...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq RLVVVSVPQSRA/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

```

Met Ala Ser Pro Phe Ser Gly Ala Leu Gln Leu Thr Asp Leu Asp Asp
-120                -115                -110

```


Phe Ile Gly Pro Ser Gln Glu Cys Ile Lys Pro Val Lys Val Glu Lys
 -105 -100 -95
 Arg Ala Gly Ser Gly Val Ala Lys Ile Arg Ile Glu Asp Asp Gly Ser
 -90 -85 -80 -75
 Tyr Phe Gln Ile Asn Gln Asp Gly Xaa Thr Arg Arg Leu Glu Lys Ala
 -70 -65 -60
 Lys Val Ser Leu Asn Tyr Cys Xaa Ala Cys Ser Gly Cys Ile Thr Ser
 -55 -50 -45
 Ala Glu Thr Val Leu Ile Thr Gln Gln Ser His Glu Glu Leu Lys Lys
 -40 -35 -30
 Val Leu Asp Ala Asn Lys Met Ala Ala Pro Ser Gln Gln Arg Leu Val
 -25 -20 -15
 Val Val Ser Val Ser Pro Gln Ser Arg Ala Ser Leu Ala Ala Arg Phe
 -10 -5 1 5
 Gln Leu Xaa Pro Thr Asp Thr Ala Arg Lys Leu Thr Ser Phe Phe Lys
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq SLVAELLLGAGSG/SH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

Met Gly Pro Val Pro Thr Ala Val Ala Gly Ala Gly Ser Arg Leu Val
 -40 -35 -30
 Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser
 -25 -20 -15
 Leu Val Ala Glu Leu Leu Leu Gly Ala Gly Ser Gly Ser His Leu Gly
 -10 -5 1
 Arg Ala Trp Ser Gly Leu Gly Ser Ser Ile Ile Glu Ala Ile Val Gly
 5 10 15 20

Val Leu Leu Thr Ile Arg Pro Ser Arg Leu Glu Pro Pro Tyr His Trp
 25 30 35
 Thr Ser Pro Ala
 40

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq QFILLGTTSVVTA/AL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly
 -20 -15 -10
 Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
 -5 1 5
 Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
 10 15 20 25
 Glu Asp Leu Lys Ser Ile Leu Ser Glu Xaa Pro Gly Lys Cys Val Pro
 30 35 40
 Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
 45 50 55
 Ser Gln Phe Val Glu Asn Cys Lys
 60 65

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq IYIICFXLPPLFS/FN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

Met Gln Val Cys Arg Cys Ile Tyr Ile Ile Cys Phe Xaa Leu Pro Pro
 -15 -10 -5

Leu Phe Ser Phe Asn
 1

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq QRLLLRFLASVIS/RK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

Met Ala Gln Arg Leu Leu Leu Arg Phe Leu Ala Ser Val Ile Ser Arg
 -15 -10 -5 1

Lys Pro Ser Gln Gly Gln Trp Ala Thr Pro His Phe Gln Ser Pro Ala
 5 10 15

Asp Pro Thr Met Gln Ser Trp Trp Pro Asp Cys Asn Thr Gln Pro Ser
 20 25 30

Pro Asp
 35

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq FLWLITRPQPVLP/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

```

Met Leu Phe Ile Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala
-40                               -35                -30                -25

Leu Ile Cys Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile
                -20                -15                -10

Thr Arg Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Xaa
                -5                1                5

```

(2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -46..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq SHMLQLLPSKALC/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

```

Met Tyr Pro Lys Trp Glu Ala Pro Val Thr Phe Cys Gln Leu Lys Arg
-45                -40                -35

Gln Lys Asp Pro Pro His Pro Ala His Ser Pro Phe Leu Gln Pro Arg
-30                -25                -20                -15

```

Phe Ser His Met Leu Gln Leu Leu Pro Ser Lys Ala Leu Cys Leu Phe
 -10 -5 1

Phe

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq LAERLGLFEELWA/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

Met Ala Leu Tyr Gln Arg Trp Arg Cys Leu Arg Leu Gln Gly Leu Gln
 -40 -35 -30

Ala Cys Arg Leu His Thr Ala Val Val Ser Thr Pro Pro Arg Trp Leu
 -25 -20 -15

Ala Glu Arg Leu Gly Leu Phe Glu Glu Leu Trp Ala Ala Gln Val Lys
 -10 -5 1

Arg Leu Ala Ser Met Ala Gln Lys Glu Pro Gln Thr
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 13.8
seq XGLLLFLLPGSLG/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

```

Met Gly Val Pro Arg Pro Gln Pro Trp Ala Xaa Gly Leu Leu Leu Phe
      -20              -15              -10

Leu Leu Pro Gly Ser Leu Gly Ala Glu Ser His Leu Ser Leu Leu Tyr
      -5              1              5

His Leu Thr Ala Val Ser Ser Pro Ala Pro Gly Thr Pro Ala Phe Trp
  10              15              20              25

Val Ser Gly Trp Leu Gly Pro Gln Gln Tyr Pro Ser Xaa
      30              35

```

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -45..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 13.4
seq LVLALXLVSAALS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

```

Met Ala Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys
-45              -40              -35              -30

Leu Leu Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro
      -25              -20              -15

Leu Val Leu Ala Leu Xaa Leu Val Ser Ala Ala Leu Ser Ser Val Val
      -10              -5              1

Ser Arg Thr Asp Ser Pro Ser Pro Thr Val Leu Asn Ser His Ile Ser
  5              10              15

Thr Pro Asn Val Asn Ala Leu Thr His Glu Asn Gln Thr Lys Pro Ser
  20              25              30              35

Ile Ser Gln Ile Ser Thr Thr Leu Pro Pro Xaa Xaa Ser Thr Lys Xaa
      40              45              50

```

Ser Gly Gly Ala Xaa Val Val Pro His Pro Ser Pro Gly
 55 60

(2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13
seq LLLVLLLVTXRS/MP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe
 -25 -20 -15

Leu Leu Leu Val Leu Leu Leu Val Thr Arg Xaa Arg Ser Met Pro Ala
 -10 -5 1

Ser Ser Pro Ala Ala Ser Ser Phe Tyr Cys Ala Ser Ser Ala Xaa Ser
 5 10 15

Arg Cys Pro Leu Ala Gly Pro Cys Arg Cys Ser Ser Pro Gly Thr Ala
 20 25 30 35

Phe Leu

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.6
seq LLLLVQLLRFLRA/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

```

Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu
  -25                      -20                      -15

Leu Leu Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu
  -10                      -5                      1

Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu
  5                      10                      15                      20

Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
  25                      30                      35

Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
  40                      45                      50

Ala Arg

```

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2
seq AFLLLVALSYTLA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

```

Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser
-20                      -15                      -10                      -5

Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp
  1                      5                      10

Thr Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
  15                      20                      25

Gly Asp Gln Leu Ile Trp Thr Arg
  30                      35

```


(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2
seq AFLLLVALSYTLA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

```

Met Ser Asn Tyr Thr Asp Ala Glu Ser Ser Phe Ser Lys Gln Glu Ile
-40                               -35                               -30                               -25

Ile Arg Val Ala Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu
-20                               -15                               -10

Val Ala Leu Ser Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly
-5                               1                               5

Ala Lys Lys Asp Thr Lys Asp Ser Arg Pro Lys Pro Pro Arg
10                               15                               20

```

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -53..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.6
seq FILLIFIAEVAA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

Met	Gln	Phe	Xaa	Thr	Trp	Ala	Thr	Ser	Ser	Ser	Gln	Pro	Ala	Leu	Trp
			-50						-45					-40	
Ser	Leu	Leu	Leu	Val	Ser	Trp	Ala	Ala	Met	Val	Leu	Arg	Leu	Arg	Ser
		-35					-30					-25			
Lys	Cys	Ala	Leu	Val	Thr	Phe	Phe	Phe	Ile	Leu	Leu	Leu	Ile	Phe	Ile
	-20					-15					-10				
Ala	Glu	Val	Ala	Ala	Ala	Val	Val	Ala	Leu	Val	Tyr	Xaa	Thr	Met	Xaa
-5					1				5					10	
Glu	His	Phe	Leu	Thr	Leu	Leu	Val	Val	Pro	Ala	Ile	Lys	Lys	Asp	Tyr
		15						20					25		
Gly	Ser	Gln	Glu	Asp	Phe	Thr	Gln	Val	Xaa	Asn	Thr	Thr	Met	Lys	Gly
		30					35					40			
Leu	Lys	Cys	Cys	Gly	Phe	Thr	Asn	Tyr	Thr	Asp	Trp				
	45					50					55				

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -28..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.5
seq LLLLVHLLRFLRA/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met	Asn	Trp	Glu	Leu	Leu	Leu	Trp	Leu	Leu	Val	Leu	Cys	Ala	Leu	Leu
			-25					-20					-15		
Leu	Leu	Leu	Val	His	Leu	Leu	Arg	Phe	Leu	Arg	Ala	Asp	Gly	Asp	Leu
		-10					-5					1			
Thr	Leu	Leu	Trp	Ala	Glu	Trp	Gln	Gly	Arg	Arg	Pro	Glu	Trp	Glu	Leu
5					10					15					20
Thr	Asp	Met	Val	Val	Trp	Val	Thr	Gly	Ala	Ser	Ser	Gly	Ile	Gly	Glu
			25						30					35	
Glu	Leu	Ala	Tyr	Gln	Leu	Ser	Lys	Leu	Gly	Xaa	Ser	Leu	Val	Leu	Ser
			40					45					50		

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5
seq LVXFSL LATAILG/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

```

Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln Leu
   -25               -20               -15

Val Xaa Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser Trp
   -10               -5               1

Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu Pro
   5               10               15               20

Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys Leu
   25               30               35

Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys
   40               45               50

Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln Glu
   55               60               65

Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe Phe
   70               75               80

Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly
   85               90               95               100

Leu

```

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3
seq VLPVILL LLLGAHP/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
 -20 -15 -10

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala
 -5 1 5 10

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Xaa Pro Ile Pro Ser
 15 20 25

Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr
 30 35 40

Ile Phe Leu Lys Phe Asp Gly Glu Arg
 45 50

(2) INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -109..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.1
seq LVLAVLFFHQLVG/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

Met Ala Ser Pro Arg Thr Val Thr Ile Val Ala Leu Ser Val Ala Leu
 - -105 -100 -95

Gly Leu Phe Phe Val Phe Met Gly Thr Ile Lys Leu Thr Pro Arg Leu
 -90 -85 -80

Ser Lys Asp Ala Tyr Ser Glu Met Lys Arg Ala Xaa Lys Ser Tyr Val
 -75 -70 -65

Arg Ala Leu Pro Leu Leu Lys Lys Met Gly Ile Asn Ser Ile Leu Leu
 -60 -55 -50

Arg Lys Ser Ile Gly Ala Leu Glu Val Ala Cys Gly Ile Val Met Thr
 -45 -40 -35 -30

Leu Val Pro Gly Arg Pro Lys Asp Val Ala Asn Phe Phe Leu Leu Leu
 -25 -20 -15

Leu Val Leu Ala Val Leu Phe Phe His Gln Leu Val Gly Asp Pro Leu
 -10 -5 1

Lys

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -38..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8
seq LLLLCALHSHIYC/IK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

Met Pro Asn Leu Ser Phe Gly Gly Leu Asp Thr Asn Gln Met Arg Val
-35 -30 -25

Asn Phe Leu Ser Val Asp Val Cys Lys Leu Leu Leu Leu Cys Ala Leu
-20 -15 -10

His Ser His Ile Tyr Cys Ile Lys Gln Ser Ala Leu Arg
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8
seq XXLLLLNVGQLLA/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

```

Met Gly Pro Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu
-55                      -50                      -45                      -40

Leu Met Met Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu
                      -35                      -30                      -25

Ser Thr Cys Ile Pro Ala Ile Val Cys Leu Xaa Xaa Leu Leu Leu Leu
                      -20                      -15                      -10

Asn Val Gly Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr
                      -5                      1                      5

Arg Lys Lys Thr Leu Ser Thr
10                      15

```

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -71..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6
seq VVXFLLLLLAXLIA/TY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

```

Met Xaa Xaa Phe Thr Asp Pro Ser Ser Val Asn Glu Lys Lys Arg Arg
-70                      -65                      -60

Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln Pro Leu Ile
-55                      -50                      -45                      -40

Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu Lys Glu Trp
                      -35                      -30                      -25

Thr Ser Lys Leu Trp His Arg Xaa Xaa Ile Val Val Xaa Phe Leu Leu
                      -20                      -15                      -10

Leu Leu Ala Xaa Leu Ile Ala Thr Tyr Tyr
-5                      1

```

(2) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.6
seq LLRGLLWXQVLCA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

```
Met Pro Leu Leu Arg Gly Leu Leu Trp Xaa Gln Val Leu Cys Ala Gly
-15                -10                -5                1

Pro Leu His Thr Glu
                5
```

(2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.4
seq AVVGCLLVPPAEA/NK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

```
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
-20                -15                -10                -5

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Xaa Cys Lys Cys Ile
                1                5                10

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
15                20                25

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
30                35                40
```


Pro
45

(2) INFORMATION FOR SEQ ID NO: 494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg
 -20 -15 -10

Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro
 -5 1 5

Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val Ser Ala Ala
 10 15 20

Phe Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile Ala Arg Ala
 25 30 35 40

Val Gly Glu Lys Arg
 45

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -108...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.9
 seq LLGLLSAEQLAEA/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

```

Met Cys Leu Leu Leu Gly Ala Thr Gly Val Gly Lys Thr Leu Leu Val
    -105                      -100                      -95

Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly Asp Leu Gly
    -90                      -85                      -80

Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu Thr Asp Ile
    -75                      -70                      -65

Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly Cys Met Gly
    -60                      -55                      -50                      -45

Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu Leu Phe Val
    -40                      -35                      -30

Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Xaa Xaa Val Gln Leu
    -25                      -20                      -15

Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser Val Leu Ile
    -10                      -5                      1

Leu Phe Asn Lys Ile Asp Asn
    5                      10
  
```

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -41...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.7
 seq LLCLGQLHHPGLG/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

```

Met Glu Leu Pro Ala Val Asn Leu Glu Ser Asp Ser Pro Arg Ser Leu
    -40                      -35                      -30

Ala Ala Asp Asn Leu Gly Leu His Cys Ile Leu Arg Leu Leu Cys Leu
  
```

-25

-20

-15

-10

Gly Gln Leu His His Pro Gly Leu Gly Arg Val Gly Cys Gly Ser Ala
 -5 1 5

Gly Leu His Arg Arg Arg
 10

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq PALILLFALGSLG/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

Met Ala Phe Leu Arg Lys Val Tyr Ser Ile Leu Ser Leu Gln Val Leu
 -50 -45 -40

Leu Thr Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser Val Arg
 -35 -30 -25 -20

Thr Phe Val His Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly
 -15 -10 -5

Ser Leu Gly Ser Gly
 1

(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

(2) INFORMATION FOR SEQ ID NO: 499:

(ii) MOLECULE TYPE: PROTEIN

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(A) NAME/KEY: sig_peptide
(B) LOCATION: -32..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.6
seq WILVLALPLTVWP/WL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

(2) INFORMATION FOR SEO ID NO: 500:

(A) LENGTH: 88 amino acids

- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.5
seq AVLLALLMAGLAL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

```
Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
-15                -10                -5                1
Pro Gly Thr Ala Leu Leu Cys Tyr Ser Trp Xaa Ala Gln Val Xaa Asn
      5                10                15
Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
      20                25                30
Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
      35                40                45
Gly Cys Ser Leu Asn Cys Val Asp Xaa Ser Gln Asp Tyr Tyr Val Gly
      50                55                60                65
Lys Lys Asn Ile Thr Cys Cys Asp
                        70
```

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq QACLLGLFALILS/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu Ser
 -15 -10 -5

Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr Leu Pro
 1 5 10 15

Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu Glu Leu Ser
 20 25 30

Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg Leu Ser Glu Leu
 35 40 45

Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln Tyr Gly Lys Tyr Leu
 50 55 60

Thr Arg
 65

(2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq LGSGGLGLSPGTSS/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Met Arg Pro Gly Gln Val Ser Leu Leu Gly Pro Asp Ala Val Ser Val
 -25 -20 -15

Leu Gly Ser Gly Leu Gly Leu Ser Pro Gly Thr Ser Ser Gly Arg Asn
 -10 -5 1

Pro Asp Pro Gly Ser Gly Pro Gly Thr Leu Pro Xaa Xaa Ser Xaa Gln
 5 10 15

Asn Pro Ser Pro Ala Pro Asp Pro Pro Pro Ala Leu Leu Leu Trp Asn
 20 25 30 35

Leu Leu Thr Gln Arg Leu Gly Thr Thr Leu Val Pro Thr Leu Cys Pro
 40 45 50

Ala Gln Thr Leu Ile Leu Cys Pro Ala Gln Thr Leu Ile Leu Cys Pro
 55 60 65

Xaa Leu Ile Pro Thr Leu Cys Pro Ala Leu Xaa Pro Val Leu Pro Xaa
70 75 80
Val Ala Leu Ser Ala Gln Pro Ser Leu Pro Ala Arg Val Gln Ser
85 90 95

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.8
seq FTSASLLLLPMSTG/MP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

Met Ile Asn Pro Ser Val Pro Ser Lys Ser Asn Ser His Pro Phe Leu
-30 -25 -20
Ser Thr Val Met Phe Thr Ser Ala Ser Leu Leu Leu Pro Met Ser Thr
-15 -10 -5
Gly Met Pro Thr Gln Asn Cys Phe Thr Pro Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -68..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7

seq IACLAWWIGGGSG/XN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

Met Ser Glu Lys Glu Xaa Asn Phe Pro Pro Leu Pro Lys Phe Ile Pro
 -65 -60 -55

Val Lys Pro Cys Phe Tyr Gln Asn Phe Ser Asp Glu Ile Pro Val Glu
 -50 -45 -40

His Gln Val Leu Val Lys Arg Ile Tyr Arg Leu Trp Met Phe Tyr Cys
 -35 -30 -25

Ala Thr Leu Gly Val Asn Leu Ile Ala Cys Leu Ala Trp Trp Ile Gly
 -20 -15 -10 -5

Gly Gly Ser Gly Xaa Asn Phe Gly Leu Ala Phe Val Trp Leu Leu Leu
 1 5 10

Phe Thr Pro Cys Gly Tyr Val Cys Trp Phe Arg Pro Val Tyr Lys Ala
 15 20 25

Phe Arg Ala Asp Ser Ser Phe Asn Phe Met Ala Leu
 30 35 40

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
 seq ILRLYFFFLQLAHS/GY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

Met Asn Pro Thr Lys Leu Ile Leu Lys Thr Ile Leu Arg Leu Tyr Phe
 -20 -15 -10

Phe Leu Gln Leu Ala His Ser Gly Tyr Thr Lys Leu Gln Lys Lys Tyr
 -5 1 5

Met Lys Ser Arg Tyr Glu Gln Val Asp Leu Val Gly Lys Met Xaa Gln
 10 15 20 25

Lys Ala Ala Thr Thr Val Xaa His Leu Ala Ile Gln Cys His Trp